

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 06:01:49 ; Search time 777.143 Seconds

(without alignments)
1462.883 Million cell updates/sec

Title: US-10-661-094-1_COPY_898_917

Perfect score: 20

Sequence: 1 ttcagcgcaccccttcggtg 20

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 120 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_in:*
3: gb_env:*
4: gb_cm:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hlg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
C 1	20	100.0	20 6 CS061876	CS061876 Sequence
2	20	100.0	614 1 AT754011	AT754011 Enterococ
3	20	100.0	1029 6 AR035505	AR035505 Sequence
4	20	100.0	1029 6 BD181846	BD181846 Polypepti
5	20	100.0	1032 6 AX085668	AX085668 Sequence
6	20	100.0	1032 6 AX110319	AX110319 Sequence
7	20	100.0	1034 6 CQ797595	CQ797595 Sequence
8	20	100.0	1218 6 AX110322	AX110322 Sequence
9	20	100.0	1237 6 AX110321	AX110321 Sequence
10	20	100.0	1237 6 AX110319	AX110319 Sequence
11	20	100.0	1241 6 AX110316	AX110316 Sequence
12	20	100.0	1249 6 AX110317	AX110317 Sequence
13	20	100.0	1263 6 AX110320	AX110320 Sequence
14	20	100.0	1265 6 AX110323	AX110323 Sequence
15	20	100.0	1269 6 AX110324	AX110324 Sequence
16	20	100.0	1272 6 AX110318	AX110318 Sequence
17	20	100.0	1768 6 EFPVANG	EFPVANG
18	20	100.0	1768 6 CQ797596	CQ797596 Sequence

19	20	100.0	1768 6 CQ797597	CQ797597 Sequence
20	20	100.0	1768 6 CS061873	CS061873 Sequence
21	20	100.0	1768 6 AX110406	AX110406 Sequence
22	20	100.0	2607 6 AR089411	AR089411 Sequence
23	20	100.0	2607 6 AR093611	AR093611 Sequence
24	20	100.0	2667 6 AR035514	AR035514 Sequence
25	20	100.0	2667 6 BD181855	BD181855 Polypepti
26	20	100.0	3946 6 AX110408	AX110408 Sequence
27	20	100.0	7225 6 AR035512	AR035512 Sequence
28	20	100.0	7225 6 BD181853	BD181853 Polypepti
29	20	100.0	10851 1 TRNVAN	TRNVAN
30	20	100.0	10851 6 AR035513	AR035513 Sequence
31	20	100.0	10851 6 BD181854	BD181854 Polypepti
32	20	100.0	10851 6 AX085648	AX085648 Sequence
33	20	100.0	17510 1 AF516335	AF516335 Enterococ
34	20	100.0	57889 1 AE017171	AE017171 Staphyloc
35	18.4	92.0	786 1 OTEPVAN2	OTEPVAN2
36	18.4	92.0	186605 9 AL606928	AL606928 Mouse DNA
37	18	90.0	399 3 DQ117337	DQ117337 Unculture
38	18	90.0	801 3 AY327227	AY327227 Unculture
39	17.4	87.0	48352 13 AY225134	AY225134 Feldmanni
40	17.4	87.0	92474 8 AC131384	AC131384 Homo sapi
41	17.4	87.0	144542 8 AC015819	AC015819 Homo sapi
42	17.4	87.0	150214 8 AC091489	AC091489 Homo sapi
43	17.4	87.0	153596 14 AC130453	AC130453 Homo sapi
44	17.4	87.0	153773 8 HUAC004020	HUAC004020 Homo sapi
45	17.4	87.0	170711 14 AC032020	AC032020 Homo sapi
46	17.4	87.0	190048 9 AL591126	AL591126 Mouse DNA
47	17.4	87.0	190123 14 AC141358	AC141358 Bos tauru
48	17.4	87.0	203643 14 AC140525	AC140525 Homo sapi
49	17.4	87.0	210236 14 AC150639	AC150639 Bos tauru
50	17.4	87.0	223891 14 AC163846	AC163846 Bos tauru
51	17	85.0	812 15 AJ717397	AJ717397 Schodonor
52	17	85.0	1087 15 AJ786400	AJ786400 Schodonor
53	17	85.0	1409 15 AY366339	AY366339 Schodonor
54	17	85.0	1409 15 AC138719	AC138719 Mus muscu
55	16.8	84.0	201 10 BV207778	BV207778 eqm2453
56	16.8	84.0	277 3 AF406375	AF406375 Unculture
57	16.8	84.0	304 3 BD058535	BD058535 Unculture
58	16.8	84.0	548 6 BX388755	BX388755 Sequence
59	16.8	84.0	638 6 BX388755	BX388755 Sequence
60	16.8	84.0	1054 1 BCY15704	BCY15704 Bacillus ci
61	16.8	84.0	1107 3 UMBSAR11	UMBSAR11 Unknown mar
62	16.8	84.0	1119 3 AY664069	AY664069 Unculture
63	16.8	84.0	1172 3 AY664067	AY664067 Unculture
64	16.8	84.0	1180 3 AY664079	AY664079 Unculture
65	16.8	84.0	1187 3 AY664092	AY664092 Unculture
66	16.8	84.0	1206 3 AY664083	AY664083 Unculture
67	16.8	84.0	1397 3 DQ071046	DQ071046 Unculture
68	16.8	84.0	1397 3 DQ071046	DQ071046 Unculture
69	16.8	84.0	1397 3 DQ071148	DQ071148 Unculture
70	16.8	84.0	1433 3 AF382131	AF382131 Unculture
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72	16.8	84.0	1959 3 DQ009251	DQ009251 Unculture
73	16.8	84.0	2311 8 BC002875	BC002875 Homo sapi
74	16.8	84.0	3121 8 HSU88154	HSU88154 Homo sapien
75	16.8	84.0	3186 8 AY882602	AY882602 Homo sapi
76	16.8	84.0	3211 6 AR077147	AR077147 Sequence
77	16.8	84.0	3211 6 AR170436	AR170436 Sequence
78	16.8	84.0	3216 6 BC010457	BC010457 Homo sapi
79	16.8	84.0	3393 8 AF547989	AF547989 Homo sapi
80	16.8	84.0	3456 8 BC069058	BC069058 Homo sapi
81	16.8	84.0	3901 6 AR077146	AR077146 Sequence
82	16.8	84.0	3901 6 AR170435	AR170435 Sequence
83	16.8	84.0	3910 8 HSU88153	HSU88153 Homo sapien
84	16.8	84.0	5000 1 ASU13677	ASU13677 Arabidosa sp
85	16.8	84.0	11521 1 AR013459	AR013459 Methanosa
86	16.8	84.0	23152 9 AL731720	AL731720 Mouse DNA
87	16.8	84.0	43190 8 AC005777	AC005777 Homo sapi
88	16.8	84.0	43190 8 AC027788	AC027788 Homo sapi
89	16.8	84.0	79995 14 AC022231	AC022231 Mus muscu
90	16.8	84.0	80419 8 AL139826	AL139826 Human DNA
91	16.8	84.0	86945 14 AC002490	AC002490 Homo sapi

C 92 16.8 84.0 94023 8 AC008720 Homo sapi
93 16.8 84.0 104771 9 AL603830
16.8 84.0 110000 15 BA000819 63
95 16.8 84.0 110000 15 AP008216_130
C 96 16.8 84.0 119227 15 CR378662 M. truncat
97 16.8 84.0 144593 15 AC021891 Genomic S
C 98 16.8 84.0 148671 14 AC120316 Homo sapi
C 99 16.8 84.0 153248 8 AC112191 Homo sapi
C 100 16.8 84.0 154353 8 AC027820 Homo sapi
C 101 16.8 84.0 154405 8 AC004990 Homo sapi
102 16.8 84.0 153043 14 AC124654 Homo sapi
C 103 16.8 84.0 166134 9 AC127734 Rattus no
104 16.8 84.0 169622 14 AC102421 Mus muscu
105 16.8 84.0 174846 14 AC141676 Apis mell
106 16.8 84.0 191766 8 AC087274 Homo sapi
107 16.8 84.0 192590 14 AC118858 Rattus no
C 108 16.8 84.0 192805 8 AC146435 Pan trogl
C 109 16.8 84.0 192963 14 AC020736 Homo sapi
C 110 16.8 84.0 193896 8 AC048387 Homo sapi
C 111 16.8 84.0 195494 8 AC091153 Homo sapi
C 112 16.8 84.0 197370 14 AC130442 Rattus no
C 113 16.8 84.0 201207 14 AC150689 Bos tauri
C 114 16.8 84.0 204620 9 AC163342 Mus muscu
115 16.8 84.0 212749 14 AC156177 Bos tauri
C 116 16.8 84.0 223613 14 AC162216 Rattus no
C 117 16.8 84.0 234160 14 AC117890 Rattus no
C 118 16.8 84.0 241475 14 AC132756 Rattus no
C 119 16.8 84.0 246246 14 AC103121 Rattus no
C 120 16.8 84.0 262124 14 AC095111 Rattus no

ALIGNMENTS

RESULT 1
LOCUS CS061876/c 20 bp DNA linear PAT 13-APR-2005
DEFINITION Sequence 4 from Patent WO2005028679.
ACCESSION CS061876
VERSION CS061876.1 GI:62553770

KEYWORDS Enterococcus faecium
SOURCE Enterococcus faecium
ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE 1
AUTHORS Dodgson, K.J.
TITLE Method and kit for identifying vancomycin-resistant enterococcus
JOURNAL Patent: WO 2005028679-A 4 31-MAR-2005;
University of Iowa Research Foundation (US); DODGSON, Kirstey Jane
(US)

FEATURES
source location/Qualifiers
1..20
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/db_xref="taxon:1352"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 TTGAGGCTCATCTTCGGTG 20
20 TTGAGGCTCATCTTCGGTG 1

RESULT 2
LOCUS AY754011 614 bp DNA linear BCT 19-JAN-2005
DEFINITION Enterococcus faecium vancomycin resistance protein A (vna) gene,
partial cds.
ACCESSION AY754011

VERSION AY754011.1 GI:57790303
KEYWORDS Enterococcus faecium
SOURCE Enterococcus faecium
ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE 1 (bases 1 to 614)
AUTHORS Khudaler, B.Y., Shafiani, S., Tewari, R. and Taneja, N.
TITLE Detection and molecular characterization of vancomycin resistance
genes from clinical strains of Enterococci

JOURNAL Unpublished
2 (bases 1 to 614)

REFERENCE Khudaler, B.Y., Shafiani, S., Tewari, R. and Taneja, N.
AUTHORS Direct Submission
TITLE Submitted (18-SEP-2004) Biotechnology, Panjab University,
Sector-14, Chandigarh, U.T 160014, India

JOURNAL location/Qualifiers

FEATURES

source 1..614
/organism="Enterococcus faecium"
/mol_type="genomic DNA"
/db_xref="taxon:1352"
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/gene="vna"
<1..>614
/gene="vna"
/codon_start=1
/transl_table=11
/product="vancomycin resistance protein A"

/protein_id="AAW56079.1"
/db_xref="GI:57790304"
/translation="LVKKNHRYEINHVDVAFSALHSGSBDISQGLFELSGIPYVC
DIQSSAICMDKSLTYIVANKNAGATPAFWINQDDPVPATFTYFPVFAFGSSFG
VKVNSADELDYVAIESARQDYSKILIEQAVSGCEVCATVAGNSAALAVESVDQIRLQY
GIFRIHQEVEPEKSENAVITVPADLSABERGRIGRTAKIKYAL"

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 614;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTGAGGCTCATCTTCGGTG 20
288 TTGAGGCTCATCTTCGGTG 307

RESULT 3
LOCUS AR035505 1029 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 3 from patent US 5871910.
ACCESSION AR035505
VERSION AR035505.1 GI:5952173

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1029)
AUTHORS Arthur, M., Dutka-Malen, S., Molina, C. and Courvalin, P.
TITLE Probes for the detection of nucleotide sequences implicated in the
expression of resistance to glycopeptides, in particular in
gram-positive bacteria

JOURNAL Patent: US 5871910-A 3 16-FEB-1999;
FEATURES location/Qualifiers
1..1029
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 1029;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 TTGAGGCTCATCTTCGGTG 20
|||||

Db 522 TTCAGGCTCATCTTCGGTG 541

RESULT 4
LOCUS BD181846
DEFINITION
BD181846 1029 bp DNA linear PAT 15-MAY-2003
Polypeptides implicated in the expression of resistance to
glycopeptides, in particular in gram-positive bacteria, nucleotide
sequence cod ing for these polypeptides and use for diagnosis.
BD181846
BD181846.1 GI:30792764
JP 2002320494-A/2.
UNIDENTIFIED
SOURCE
ORGANISM
unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 1029)
TITLE Arthur M., Duktamalen, S., Molinas, C. and Courvalin, P.
JOURNAL Polypeptides implicated in the expression of resistance to
glycopeptides, in particular in gram-positive bacteria, nucleotide
sequence cod ing for these polypeptides and use for diagnosis
PATENT: JP 2002320494-A 2 05-NOV-2002;
INSTITUT PASTEUR

COMMENT
OS Bacteria
PN JP 2002320494-A/2
PD 05-NOV-2002
PR 21-FEB-2002 JP 2002045484
PR 31-OCT-1990 FR 90/13579
PI MICHEL, ARTHUR, SYLVIE DUKTA-MALEN, CATHERINE MOLINAS, PATRICE
COURVALIN

PC C12N15/09, C07K14/315, C07K16/12, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12Q1/04, C12Q1/68, G01N33/53, G01N33/566, G01N33/569//C12P21/08,
PC (C12Q1/04, C12R1/01), (C12Q1/68, C12R1/01), C12N15/00, C12N5/00 CC
Polypeptides implicated in the expression of resistance to CC
glycopeptides.
CC in particular in gram-positive bacteria, nucleotide sequence
CC cod ing for
CC these polypeptides and use for diagnosis
FH Key Location/Qualifiers
FT source 1. 1029
FT /organism="Bacteria".

FEATURES
source 1. 1029
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 1029;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAGGCTCATCTTCGGTG 20
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Db 522 TTCAGGCTCATCTTCGGTG 541

RESULT 5
LOCUS AX085668
DEFINITION
AX085668 1032 bp DNA linear PAT 09-MAR-2001
Sequence 21 from Patent WO0112803.
AX085668
AX085668.1 GI:13275654

KEYWORDS
SOURCE
ORGANISM
Enterococcus faecium
Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE
AUTHORS 1
TITLE Inouye, R.T., Torres-Viera, C., Moellerling, R., Gold, H. and
Ellopoulos, G.M.
JOURNAL Methods and compositions for restoring antibiotic susceptibility in
glycopeptide-resistant Enterococcus

JOURNAL Patent: WO 0112803-A 21 22-FEB-2001;
Beth Israel Deaconess Medical Center, Inc. (US)

FEATURES
source 1. 1032
Location/Qualifiers
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/db_xref="taxon:1352"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 1032;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAGGCTCATCTTCGGTG 20
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Db 522 TTCAGGCTCATCTTCGGTG 541

RESULT 6
LOCUS AX111560
DEFINITION
AX111560 1032 bp DNA linear PAT 29-MAY-2002
Sequence 2293 from Patent WO0123604.
AX111560
AX111560.1 GI:13927852

KEYWORDS
SOURCE
ORGANISM
Enterococcus faecium
Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE
AUTHORS 1
TITLE Bergeron, M.G., Boleslanc, M., Huletsky, A., m Nard, C., Ouellette, M.,
Picard, F.J. and Roy, P.H.
JOURNAL Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
PATENT: WO 0123604-A 2293 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
Location/Qualifiers
source 1. 1032
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/mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAGGCTCATCTTCGGTG 20
|||||
Db 522 TTCAGGCTCATCTTCGGTG 541

RESULT 7
LOCUS CQ797595
DEFINITION
CQ797595 1034 bp DNA linear PAT 20-APR-2004
Sequence 9 from Patent EP1408120.
CQ797595
CQ797595.1 GI:46425887

KEYWORDS
SOURCE
ORGANISM
Enterococcus faecium
Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE
AUTHORS 1
TITLE Cockerill, F.R. and Sloan, J.M.
JOURNAL Detection of vancomycin-resistant Enterococcus spp
PATENT: EP 1408120-A 9 14-APR-2004;
MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
Location/Qualifiers
source 1. 1034
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"

ORIGIN /db_xref="taxon:1352"

Query Match 100.0%; Score 20; DB 6; Length 1034;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAGGCTCATCTTCGGTG 20
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522 TTCAGGCTCATCTTCGGTG 541

RESULT 8 AX110322 1218 bp DNA linear PAT 29-MAY-2002
LOCUS AX110322
DEFINITION Sequence 1055 from Patent WO0123604.
ACCESSION AX110322
VERSION AX110322.1 GI:13926614
KEYWORDS
SOURCE Enterococcus gallinarum
ORGANISM Enterococcus gallinarum
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE 1
AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
JOURNAL for detection of microorganisms
PATENT: WO 0123604-A 1055 05-APR-2001;
INfectio Diagnostic (I.D.I.) INC. (CA)
FEATURES
source Location/Qualifiers
1. 1218
/organism="Enterococcus gallinarum"
/mol_type="unassigned DNA"
/strain="R684"
/db_xref="taxon:1352"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAGGCTCATCTTCGGTG 20
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596 TTCAGGCTCATCTTCGGTG 615

RESULT 9 AX110321 1232 bp DNA linear PAT 29-MAY-2002
LOCUS AX110321
DEFINITION Sequence 1054 from Patent WO0123604.
ACCESSION AX110321
VERSION AX110321.1 GI:13926613
KEYWORDS
SOURCE Enterococcus faecalis
ORGANISM Enterococcus faecalis
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE 1
AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
JOURNAL for detection of microorganisms
PATENT: WO 0123604-A 1054 05-APR-2001;
INfectio Diagnostic (I.D.I.) INC. (CA)
FEATURES
source Location/Qualifiers
1. 1232
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/db_xref="taxon:1351"
/note="R610"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 1232;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAGGCTCATCTTCGGTG 20
|||||
606 TTCAGGCTCATCTTCGGTG 625

RESULT 10 AX110319 1237 bp DNA linear PAT 29-MAY-2002
LOCUS AX110319
DEFINITION Sequence 1052 from Patent WO0123604.
ACCESSION AX110319
VERSION AX110319.1 GI:13926611
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE 1
AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
JOURNAL for detection of microorganisms
PATENT: WO 0123604-A 1052 05-APR-2001;
INfectio Diagnostic (I.D.I.) INC. (CA)
FEATURES
source Location/Qualifiers
1. 1237
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/mol_type="unassigned DNA"
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/db_xref="taxon:1352"

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 11 AX110316 1241 bp DNA linear PAT 29-MAY-2002
LOCUS AX110316
DEFINITION Sequence 1049 from Patent WO0123604.
ACCESSION AX110316
VERSION AX110316.1 GI:13926608
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE 1
AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
JOURNAL for detection of microorganisms
PATENT: WO 0123604-A 1049 05-APR-2001;
INfectio Diagnostic (I.D.I.) INC. (CA)
FEATURES
source Location/Qualifiers
1. 1241
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/strain="R690"
/db_xref="taxon:1352"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 1241;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 16
AX110318 1272 bp DNA linear PAT 29-MAY-2002
LOCUS Sequence 1051 from Patent WO0123604.
DEFINITION AX110318
ACCESSION AX110318
VERSION AX110318.1 GI:13926610
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.
REFERENCE 1
AUTHORS Bergeron,M.G., Bolesinc,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
JOURNAL Patent: WO 0123604-A 1051 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES
source location/Qualifiers
1. 1272
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/strain="R481"
/db_xref="taxon:1352"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 1272;
Best Local Similarity 100.0%; Pred. No. 7.3; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGAGGCTCATCCTTCGGTG 20
598 TTGAGGCTCATCCTTCGGTG 617
Db

RESULT 17
EFPVANAG 1768 bp DNA linear BCT 17-JUN-1991
LOCUS E.faecium plasmid p1816 vana gene for VANA ligase.
DEFINITION X66895
ACCESSION X66895.1 GI:43335
VERSION D-alanyl-D-alanine ligase; VANA glycopeptide resistance protein;
KEYWORDS vancomycin resistance.
SOURCE Enterococcus faecium
ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.
REFERENCE 1 (bases 1 to 1768)
AUTHORS Dutka-Malen,S., Molinas,C., Arthur,M. and Courvalin,P.
TITLE The VANA glycopeptide resistance protein is related to
D-alanyl-D-alanine ligase cell wall biosynthesis enzymes
JOURNAL Mol. Gen. Genet. 224 (3), 364-372 (1990)
PUBMED 2266943
REFERENCE 2 (bases 1 to 1768)
AUTHORS Dutka-Malen,S.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-1991) S. Dutka-Malen, Institut Pasteur, Unile des
Agents Antibacteriens, 28 rue du Dr Roux, Paris Cedex 15, France
FEATURES
source location/Qualifiers
1. 1768
/organism="Enterococcus faecium"
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/strain="BM4147"
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377..1408
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377..1408
/codon_start=1
/evidence=experimental
/transl_table=11

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/protein_id="CAA40215.1"
/db_xref="GI:43336"
/db_xref="GOA:P25051"
/db_xref="UniProt/Swiss-Prot:P25051"
/translation="MNRIRVAILFGCCSEEHVSVKSAIEIANKIKCEPLVIGIT
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RLIVLAKG"
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Best Local Similarity 100.0%; Pred. No. 7.4; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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898 TTGAGGCTCATCCTTCGGTG 917
Db

RESULT 18
CQ797596 1768 bp DNA linear PAT 20-APR-2004
LOCUS Sequence 10 from Patent EP1408120.
DEFINITION CQ797596
ACCESSION CQ797596.1 GI:46425888
VERSION CQ797596.1 GI:46425888
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.
REFERENCE 1
AUTHORS Cockrell,I.F.R. and Sloan,L.M.
TITLE Detection of vancomycin-resistant Enterococcus spp
JOURNAL Patent: EP 1408120-A 10 14-APR-2004;
MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
FEATURES
source location/Qualifiers
1. 1768
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/db_xref="taxon:1352"
/note="vana sequence"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 1768;
Best Local Similarity 100.0%; Pred. No. 7.4; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGAGGCTCATCCTTCGGTG 20
898 TTGAGGCTCATCCTTCGGTG 917
Db

RESULT 19
CQ797597 1768 bp DNA linear PAT 20-APR-2004
LOCUS Sequence 11 from Patent EP1408120.
DEFINITION CQ797597
ACCESSION CQ797597.1 GI:46425889
VERSION CQ797597.1 GI:46425889
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.
REFERENCE 1
AUTHORS Cockrell,I.F.R. and Sloan,L.M.
TITLE Detection of vancomycin-resistant Enterococcus spp
JOURNAL Patent: EP 1408120-A 11 14-APR-2004;
MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
FEATURES
source location/Qualifiers

source 1..1768
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/mol_type="unassigned DNA"
/db_xref="taxon:1352"
/note="Vana sequence"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 1768;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAGGCTCATCTTCGGTG 20
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898 TTCAGGCTCATCTTCGGTG 917

RESULT 20
CS061873 1768 bp DNA linear PAT 13-APR-2005
DEFINITION Sequence 1 from Patent WO2005028679.
ACCESSION CS061873
VERSION CS061873.1 GI:62553767
KEYWORDS Enterococcus faecium
SOURCE Enterococcus faecium
ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE 1
AUTHORS Dodgson, K.J.
TITLE Method and kit for identifying vancomycin-resistant enterococcus
JOURNAL Patent: WO 2005028679-A 1 31-MAR-2005;
University of Iowa Research Foundation (US); DODGSON, Kirsty Jane
(US)

FEATURES
source 1..1768
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/db_xref="taxon:1352"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 1768;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAGGCTCATCTTCGGTG 20
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898 TTCAGGCTCATCTTCGGTG 917

RESULT 21
AX110406 1768 bp DNA linear PAT 29-MAY-2002
LOCUS AX110406
DEFINITION Sequence 1139 from Patent WO0123604.
ACCESSION AX110406
VERSION AX110406.1 GI:13926698
KEYWORDS Enterococcus faecium
SOURCE Enterococcus faecium
ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE 1
AUTHORS Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
Picard, F.J., and Roy, P.H.
TITLE Highly conserved genes and their use to generate probes and primers
JOURNAL for detection of microorganisms
Patent: WO 0123604-A 1139 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
Location/Qualifiers
1..1768
/organism="Enterococcus faecium"
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/strain="BM4147"
/db_xref="taxon:1352"

FEATURES
source

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 1768;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAGGCTCATCTTCGGTG 20
|||||
898 TTCAGGCTCATCTTCGGTG 917

RESULT 22
AR089411 2607 bp DNA linear PAT 07-SEP-2000
LOCUS AR089411
DEFINITION Sequence 170 from patent US 5994066.
ACCESSION AR089411
VERSION AR089411.1 GI:10016168
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1
AUTHORS Bergeron, M.G., Picard, F.J., Ouellette, M., and Roy, P.H.
TITLE Species-specific and universal DNA probes and amplification primers
JOURNAL to rapidly detect and identify common bacterial pathogens and
associated antibiotic resistance genes from clinical specimens for
routine diagnosis in microbiology laboratories
Patent: US 5994066-A 170 30-NOV-1999;
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 2607;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCAGGCTCATCTTCGGTG 20
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1483 TTCAGGCTCATCTTCGGTG 1502

RESULT 23
AR093611 2607 bp DNA linear PAT 08-SEP-2000
LOCUS AR093611
DEFINITION Sequence 170 from patent US 6001564.
ACCESSION AR093611
VERSION AR093611.1 GI:10020360
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 2607)
AUTHORS Bergeron, M.G., Ouellette, M., and Roy, P.H.
TITLE Species specific and universal DNA probes and amplification primers
JOURNAL to rapidly detect and identify common bacterial pathogens and
associated antibiotic resistance genes from clinical specimens for
routine diagnosis in microbiology laboratories
Patent: US 6001564-A 170 14-DEC-1999;
Location/Qualifiers
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/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 2607;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1483 TTCAGGCTCATCTTCGGTG 1502

RESULT 24
AR035514
LOCUS AR035514 2667 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 17 from patent US 5871910.
ACCESSION AR035514
VERSION AR035514.1 GI:5952182
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
/organism="unknown"
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ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 2667;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCAGGCTCATCTTCGGTG 20
Db 1546 TTCAGGCTCATCTTCGGTG 1565

RESULT 25
BD181855
LOCUS BD181855 2667 bp DNA linear PAT 15-MAY-2003
DEFINITION Polypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nucleotide sequence coding for these polypeptides and use for diagnosis.
ACCESSION BD181855
VERSION BD181855.1 GI:30792773
KEYWORDS JP 2002320494-A/11.
SOURCE unidentified
ORGANISM unidentified
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Bacteria
PN JP 2002320494-A/11
PD 05-NOV-2002
PR 21-FEB-2002 JP 2002045484
PR 31-OCT-1990 FR 90/13579
PI MICHEL, ARTHUR, SYLVIE DUKTA-MALEN, CATHERINE MOLINAS, PATRICE COURVALIN
PC C12N15/09, C07K14/315, C07K16/12, C12N1/15, C12N1/19, C12N1/21, PC C12N5/10,
PC C12Q1/04, C12Q1/68, G01N33/53, G01N33/566, G01N33/569//C12P21/08, PC C12Q1/04, C12R1/01, (C12Q1/68, C12R1/01), C12N15/00, C12N5/00 CC Polypeptides implicated in the expression of resistance to CC glycopeptides, in particular in gram-positive bacteria, nucleotide sequence coding for these polypeptides and use for diagnosis
CC in particular in gram-positive bacteria, nucleotide sequence coding for these polypeptides and use for diagnosis
CC Key Location/Qualifiers
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FT /organism="Bacteria".
FEATURES
source Location/Qualifiers
1.2667

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 2667;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCAGGCTCATCTTCGGTG 20
Db 1546 TTCAGGCTCATCTTCGGTG 1565

RESULT 26
AX110408
LOCUS AX110408 3946 bp DNA linear PAT 29-MAY-2002
DEFINITION Sequence 1141 from Patent W00123604.
ACCESSION AX110408
VERSION AX110408.1 GI:13926700
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
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/db_xref="taxon:1352"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 3946;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCAGGCTCATCTTCGGTG 20
Db 1483 TTCAGGCTCATCTTCGGTG 1502

RESULT 27
AR035512
LOCUS AR035512 7225 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 15 from patent US 5871910.
ACCESSION AR035512
VERSION AR035512.1 GI:5952180
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
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ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 7225;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCAGGCTCATCTTCGGTG 20
Db 1483 TTCAGGCTCATCTTCGGTG 1502

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAGGCTCATCTTCGGTG 20
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5044 TTCAGGCTCATCTTCGGTG 5063

RESULT 28
BD181853

LOCUS BD181853 7225 bp DNA linear PAT 15-MAY-2003

DEFINITION Polypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nucleotide sequence cod ing for these polypeptides and use for diagnosis.

ACCESSION BD181853.1 GI:30792771

VERSION BD181853

KEYWORDS JP 2002320494-A/9.

SOURCE unidentified

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 7225)
Arthur, M., Dukarmalen, S., Molinas, C. and Courvaillin, P.
Polypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nucleotide sequence cod ing for these polypeptides and use for diagnosis
Patent: JP 2002320494-A 9 05-NOV-2002;

JOURNAL INSTITUT PASTEUR

COMMENT OS Bacteria
PN JP 2002320494-A/9
PD 05-NOV-2002
PF 21-FEB-2002 JP 2002045484
PR 31-OCT-1990 FR 90/13579
PI MICHEL, ARTHUR, SYLVIE DUKTA-MALEN, CATHERINE MOLINAS, PATRICE PI COURVAILLIN

PC C12N15/09, C07K14/315, C07K16/12, C12N1/15, C12N1/19, C12N1/21, PC C12N5/10.
PC C1201/04, C1201/68, G01N33/53, G01N33/566, G01N33/569, C12P21/08, PC (C1201/04, C12R1:01), (C1201/68, C12R1:01), C12N15/00, C12N5/00 CC Polypeptides implicated in the expression of resistance to CC glycopeptides, in particular in gram-positive bacteria, nucleotide sequence cod ing for these polypeptides and use for diagnosis
CC these polypeptides and use for diagnosis
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FT source 1..7225
FT location/Qualifiers
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/db_xref="taxon:32644"

FEATURES source

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCAGGCTCATCTTCGGTG 20
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5044 TTCAGGCTCATCTTCGGTG 5063

RESULT 29
TRAVAN

LOCUS TRAVAN 10851 bp DNA linear BCT 20-JUN-2002

DEFINITION Enterococcus faecium transposon Tn1546 transposase, resolvable, vanX (vanX), vanS (vanS), vanM (vanM), vanA (vanA), vanZ (vanZ), vanY (vanY), and tetracycline resistance protein (vanZ) genes, complete cds.

ACCESSION M97297

VERSION M97297.1 GI:155036

KEYWORDS Enterococcus faecium

SOURCE Enterococcus faecium

ORGANISM

REFERENCE 1 (bases 1 to 10851)
Arthur, M., Molinas, C., Depardieu, F. and Courvaillin, P.
Characterization of Tn1546, a Tn3-related transposon conferring glycopeptide resistance by synthesis of decapeptide peptidoglycan precursors in Enterococcus faecium BM4147
J. Bacteriol. 175 (1), 117-127 (1993)

JOURNAL PUBMED 8380148

REFERENCE 2 (bases 1 to 10851)
Arthur, M., Depardieu, F., Molinas, C., Reynolde, P. and Courvaillin, P.
The vanZ gene of Tn1546 from Enterococcus faecium BM4147 confers resistance to tetracycline
Gene 154 (1), 87-92 (1995)

JOURNAL PUBMED 7867956

FEATURES source

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CDS

CDS

gene

CDS

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SDGKMQAGVSLHADNPHYGKAGATTYRPTSDQSSYTKI IHTNSDAILHVD
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/db_xref="GI:155039"
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          /db_xref="GI:801884"
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ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 10851;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 TTCAAGCTCATCCTTCGGTG 20
Db 7500 TTCAAGCTCATCCTTCGGTG 7519

RESULT 30
AR035513 AR035513 10851 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 16 from patent US 5871910.
DEFINITION AR035513
ACCESSION AR035513
VERSION AR035513.1 GI:5952181
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 10851)
Arthur M., Dutka-Mallen, S., Molinas, C. and Courvalin, P.
TITLE Probes for the detection of nucleotide sequences implicated in the
expression of resistance to glycopeptides, in particular in
gram-positive bacteria
FEATURES
JOURNAL Patent: US 5871910-A 16 16-FEB-1999;
LOCATION/Qualifiers
SOURCE 1..10851
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 10851;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 TTCAAGCTCATCCTTCGGTG 20
Db 7500 TTCAAGCTCATCCTTCGGTG 7519

RESULT 31
BD181854
LOCUS 10851 bp DNA linear PAT 15-MAY-2003
DEFINITION Polypeptides implicated in the expression of resistance to
glycopeptides, in particular in gram-positive bacteria, nucleotide
sequence coding for these polypeptides and use for diagnosis.
ACCESSION BD181854
VERSION BD181854.1 GI:30792772
KEYWORDS UP 2002320494-A/10.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 10851)
Arthur M., Dutka-Mallen, S., Molinas, C. and Courvalin, P.
TITLE Polypeptides implicated in the expression of resistance to
glycopeptides, in particular in gram-positive bacteria, nucleotide
sequence coding for these polypeptides and use for diagnosis

```

JOURNAL Patent: JP 2002320494-A 10 05-NOV-2002;
INSTITUT PASTEUR
OS Bacteria
PN JP 2002320494-A/10
PD 05-NOV-2002
PF 21-FEB-2002 JP 2002045484
PR 31-OCT-1990 FR 90/13579
PI MICHEL ARTHUR, SYLVIE DURTA-MALIEN, CATHERINE MOLINAS, PATRICE PI
COURVALIN
PC C12N15/09, C07K14/315, C07K16/12, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C1201/04, C1201/68, G01N33/53, G01N33/566, G01N33/569//C12P21/08,
PC C1201/04, C12R1:01, C1201/68, C12R1:01, C12N15/00, C12N5/00 CC
Polypeptides implicated in the expression of resistance to CC
glycopeptides,
CC in particular in gram-positive bacteria, nucleotide sequence
CC coding for
CC these polypeptides and use for diagnosis
PH key Location/Qualifiers
FT source 1..10851
FT Location/Qualifiers
FT /organism='Bacteria'.
FEATURES
source 1..10851
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 10851;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTCAGGCTCATCTTCGGTG 20
|||||
Db 7500 TTCAGGCTCATCTTCGGTG 7519
|||||
RESULT 32
AX085648 10851 bp DNA linear PAT 09-MAR-2001
LOCUS
DEFINITION Sequence 1 from Patent WO0112803.
ACCESSION AX085648
VERSION AX085648.1 GI:13275634
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.
REFERENCE
1 Inouye, R.T., Torres-Viera, C., Moellering, R., Gold, H. and
Bilopoulos, G.M.
Methods and compositions for restoring antibiotic susceptibility in
glycopeptide-resistant Enterococcus
Patent: WO 0112803-A 1 22-FEB-2001;
Beth Israel Deaconess Medical Center, Inc. (US)
FEATURES
source 1..10851
/organism='Enterococcus faecium'
/mol_type='unassigned DNA'
/db_xref='taxon:1352'
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 10851;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTCAGGCTCATCTTCGGTG 20
|||||
Db 7500 TTCAGGCTCATCTTCGGTG 7519
|||||
RESULT 33
AF516335

LOCUS AF516335 17510 bp DNA linear BCT 28-AUG-2002
DEFINITION Enterococcus faecium plasmid pUW786 multiple antibiotic resistance
gene cluster, complete sequence.
ACCESSION AF516335
VERSION AF516335.1 GI:21886737
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.
REFERENCE
1 (bases 1 to 17510)
Werner, G., Klare, I. and Witte, W.
Multi-resistance gene cluster on a plasmid in a clinical isolate of
Enterococcus faecium
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 17510)
Werner, G.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-2002) Wernigerode Branch, Robert Koch Institute,
Burgstr. 37, Wernigerode 38855, Germany
FEATURES
source 1..17510
/organism='Enterococcus faecium'
/mol_type='genomic DNA'
/isolate='UW786'
/db_xref='taxon:1352'
/plasmid='pUW786'
CDS
1..532
/codon_start=2
/transl_table=11
/product='putative resolvase'
/protein_id='AAW77881.1'
/db_xref='GI:21886738'
/translation='PSROFQOLNEIGMDIIEBKVGATKORLOKYLDDIARDIIT
VYDILRIRISNODLPELINDIRKASLSKDTWLDSENPYSQSLTIWAGVNO
LARDLIRKORSGIHLAKSGSKRGRLKTHKNGMNAVALYREGMTVNOICRIT
NSRASLYRKLSSEVNN'
repeat_region
1..532
/transposon='Tn1546'
746..1441
/gene='vanR'
746..1441
/gene='vanR'
/note='regulator of two-component regulatory system'
/codon_start=1
/transl_table=11
/product='cytoplasmic regulator'
/protein_id='AAW77882.1'
/db_xref='GI:21886739'
/translation='MSDKILIVDDHRIADIVELIKNENTVPRYTTAAALAECDIK
SEIDLAIDIMPGTSGITTCQKIRDTPTPIIMLTGKQTEVDKLTGLTGADYITK
PPEPHELARVAQQLRRYKSGVKGQENRVVHGLVYNNVTHCYLNEQSLSTPT
EESILRLICEKNGVNVSEILFHEIWGDEYFSKNNITIVHRLREKMDTIDNPKY
IKTWGVGKTBK'
1419..1463
/gene='vans'
1419..1463
/allele='vans''
/allele='vans''
/codon_start=1
/transl_table=11
/product='truncated protein kinase'
/protein_id='AAW77883.1'
/db_xref='GI:21886740'
/translation='WVILKXKKXTTPN'
2787..3755
/gene='vanH'
2787..3755
/gene='vanH'
/codon_start=1
/transl_table=11
/product='pyruvate dehydrogenase'

[illegible]

REFERENCE 1 (bases 1 to 57889)
AUTHORS Gill,S., Kolonay,J., Shetty,J., Tenover,F. and Weigel,L.
TITLE Sequence of the Michigan vancomycin-resistant *Staphylococcus aureus* plasmid
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 57889)
AUTHORS Gill,S., Kolonay,J., Shetty,J., Tenover,F. and Weigel,L.
TITLE Direct Submission
JOURNAL Submitted (30-JUL-2003) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA

FEATURES
source
1..57889
/organism="Staphylococcus aureus"
/mol_type="genomic DNA"
/db_xref="taxon:1280"
/plasmid="pLM043"
101..1060
/gene="tepa"
/locus_tag="VRA0001"
101..1060
/gene="tepa"
/locus_tag="VRA0001"
/locus_tag="VRA0001"
/note="similar to GP:3676426, and GP:1041637; identified by sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="replication initiator protein"
/protein_id="AAQ17124.1"
/db_xref="GI:33390918"
/translation="MSKQPTVYENYKERFYQLPVFPPTNPYKLSNDKAVATIRDLQSLKNNWIDTEGIVPIYVAVLEVLINCGKKKTKIKKELENDVLLIQKQGLNKPMLTLKPAITKNDIYRIDAESEVALLDDKVSQGHVQCKQKQTSRNVKRTBLEMSKGYNDTDTIDTDFIDTSENMMNNMNDTQNSHNSHNFENIDHESLKYIEIOLPBLIKSYINPSEYBEVKISVILKAKKSFNKKYDTFMLEDIDEEILLVLRFRGYIYKKQEVANMGGYLMRSIIAIEEMHSTIRRRMMENPLSLFN"
1179..1853
/locus_tag="VRA0002"
1179..1853
/locus_tag="VRA0002"
/note="similar to GP:1383313, and SP:P19380; identified by sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="IS43Iec transposase"
/protein_id="AAQ17125.1"
/db_xref="GI:33390919"
/translation="WNYFRYKQPNQVITVAVGYTLRYALSYRDISILLRGKGVNHHSTYRWQVEYAPILYQIMKKKKKAYKRIIDETIKIKGMSYLYRAIDAEHTLIDILWLRKQRDNHSAVAFIKRLIKQFGKPOKVTDDAPSTKAMKVIKAPLADGCHTSKYLNMLIEQDHRHIIKVRKTRYQSINTAKMLKIECIYALYKQNRSLQIYGFPCHEI SIMLAS"
Complement (1885..2307)
/locus_tag="VRA0003"
Complement (1885..2307)
/locus_tag="VRA0003"
/note="similar to GP:4105402; identified by sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="conserved hypothetical protein"
/protein_id="AAQ17126.1"
/db_xref="GI:33390920"
/translation="MAKOIIVDTSDLSHEYLAKOHNIHVIPLSLTIDKSYTDQVDSSEYIDHENDADVKSOPPIGRPIETRYEOLADQDEIISIHLSGLSGVTNVAQASHMDGNITVYIDSKSISFGIGYOIKOYVALVLLQSKRT"
Complement (2317..2802)
/gene="dfrA"
/locus_tag="VRA0004"
Complement (2317..2802)
/gene="dfrA"
/locus_tag="VRA0004"
/note="similar to GP:1383309, and SP:P11045; identified

by sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="trimethoprim resistant dihydrofolate reductase"
/protein_id="AAQ17127.1"
/db_xref="GI:33390921"
/translation="WTSIIVADHKQRYIGYQNGQPMHLPNDLKHIKOLTTGNTLVNARKTPNSIGKPLPNRRNVALLTNQASFRHSGVDVNSIDETIKELSGVTFGGQTLVAMIDQVDMYITVIDSKFQGDTPFPPTTFENNEVSSVEGQDDEKNTIPHTFLVLRGSK"
Complement (2844..3800)
/gene="thyA"
/locus_tag="VRA0005"
Complement (2844..3800)
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/locus_tag="VRA0005"
/note="similar to SP:P13954, and SP:P00463; identified by sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="thymidylate synthase"
/protein_id="AAQ17128.1"
/db_xref="GI:33390922"
/translation="WYNPDEAYHGLCEBILBIGNRDRTHVTGTSKFGHQLRFDLTKEPPLITTKYSPFLVATELWFLKGDITNIOYLAKNNINWBNAFENYVQSDDYHGPDMTDFGRHSQODPEPNEQYKEKKKREKRLINDDAFAKKYGLGAVYQKQRMEDENGNHTDQLKSVYQOIKTNPNSRRIIVSANMPTBIDSMALPCHTNGQFTVQSGKLNCLYQSRADIFLQVFPFNIAVYALLTHLVAKEGGLVEGFTHFGDAHLYSNHMDAHTQLSRSYLPQDKINTDKSIFDINVEDLIEIVESHPAIKAPIAV"
3914..4588
/locus_tag="VRA0006"
3914..4588
/locus_tag="VRA0006"
/note="similar to SP:P14506, and SP:P19380; identified by sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="IS43Iec transposase"
/protein_id="AAQ17129.1"
/db_xref="GI:33390923"
/translation="WNYFRYKQPNQVITVAVGYTLRYALSYRDISILLRGKGVNHHSTYRWQVEYAPILYQIMKKKKKAYKRIIDETIKIKGMSYLYRAIDAEHTLIDILWLRKQRDNHSAVAFIKRLIKQFGKPOKVTDDAPSTKAMKVIKAPLADGCHTSKYLNMLIEQDHRHIIKVRKTRYQSINTAKMLKIECIYALYKQNRSLQIYGFPCHEI SIMLAS"
Complement (4697..4885)
/gene="araA"
/locus_tag="VRA0007"
Complement (4697..4885)
/gene="araA"
/locus_tag="VRA0007"
/note="similar to GP:21623785; identified by sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="regulator of transfer gene AraA"
/protein_id="AAQ17130.1"
/db_xref="GI:33390924"
/translation="WNNNEENSVPFGKKKVSILHLVDPDMKDBELIKVAKQKPDVNSQAGREILKGLKQIKSNK"
5057..6031
/gene="traA"
/locus_tag="VRA0008"
5057..6031
/gene="traA"
/locus_tag="VRA0008"
/locus_tag="VRA0008"
/note="similar to GP:3676435, GB:X15505, GB:D45417, SP:P15951, SP:P35030, and PID:37460; identified by sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="traA"
/protein_id="AAQ17131.1"

LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
LOCUS	OTPDVANAM2	786 bp	DNA	linear	BCT 18-APR-2005				
DEFINITION	O.turdata Plasmid DNA for vancomycin resistance protein.								
VERSION	X79049								
KEYWORDS	X79049.1 GI:479085								
SOURCE	vanA2 gene; vancomycin resistance.								
ORGANISM	Oerskovia turdata								
REFERENCE	Oerskovia turdata								
AUTHORS	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;								
TITLE	Micrococciaceae; Cellulomonadaceae; Oerskovia.								
JOURNAL	1 (bases 1 to 786)								
	Dutka-Malen, S., Molinas, C., Arthur, M. and Courvalin, P.								
	The vanA glycopeptide resistance protein is related to								
	D-alanyl-D-alanine ligase cell wall biosynthesis enzymes								
	Mol. Gen. Genet. 224 (3), 364-372 (1990)								

PUBMED	2266943	
REFERENCE	2	
AUTHORS	Power, E.G., Abdulla, Y.H., Taisania, H.G., Spice, W., Athithan, S. and French, G.J.	
TITLE	vana genes in vancomycin-resistant clinical isolates of <i>Oerskovia turbata</i> and <i>Arcanobacterium</i> (<i>Corynebacterium</i>) <i>haemolyticum</i>	
JOURNAL	J. Antimicrob. Chemother. 36 (4), 595-606 (1995)	
PUBMED	8591934	
REFERENCE	3 (bases 1 to 786)	
AUTHORS	Power, E.G.M.	
TITLE	Direct Submission	
JOURNAL	Submitted (28-APR-1994) E.G.M. Power, UMDS, Dept of Microbiology, Guy's Campus, London Bridge, London SE1 9RT, UK	
FEATURES	Location/Qualifiers	
source	1..786	
	/organism="Oerskovia turbata"	
	/mol_type="genomic DNA"	
	/isolate="92"	
	/db_xref="taxon:1713"	
gene	<1..>786	
	/gene="vana2"	
	<1..>786	
CDS	/gene="vana2"	
	/codon_start=3	
	/transl_table=11	
	/protein_id="CAA55651.1"	
	/db_xref="GI:479086"	
	/db_xref="GOA:Q51332"	
	/db_xref="InterPro:IPR000291"	
	/db_xref="InterPro:IPR011095"	
	/db_xref="InterPro:IPR01127"	
	/db_xref="InterPro:IPR011761"	
	/db_xref="UniProt/TrEMBL:Q51332"	
	/translation="KSGVWRCPEPCPEAWENDNCYSALSPDKKHGLLYKQNEHYITNHDVAISLHGKSGEDSGIQGLFELSGIFPVGDIQSSALICMDKSLTYIVAKNAGLIA TPFWVINKODRPVAATSTYVFGKPARSGSSFGVKVNSADELDVATIESRQYDSKIKLIRAVSGCEVCAVIGNSAALVAGEVDRIQGIPIRHOEVEPEKGSNAVITVPA DLSAERNGRIQETGKTKIYKALGCGRLARVDMFLQDNRIYLNQ"	
misc_difference	361	
	/gene="vana2"	
	/note="vana equivalent position 867"	
	/citation=[1]	
	/replace="t"	
misc_difference	374	
	/gene="vana2"	
	/note="vana equivalent position 880"	
	/citation=[1]	
	/replace="t"	
misc_difference	379	
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	/note="vana equivalent position 885"	
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	/note="vana equivalent position 916"	
	/citation=[1]	
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	/gene="vana2"	
	/note="vana equivalent position 1048"	
	/citation=[1]	
	/replace="c"	
misc_difference	697	
	/gene="vana2"	
	/note="vana equivalent position 1203"	
	/citation=[1]	
	/replace="c"	
ORIGIN		
Query Match	92.0%	Score 18.4; DB 1; Length 786;
Best Local Similarity	95.0%	Pred. No. 58;
Matches 19; Conservative	0; Mismatches 1; Indels 0; Gaps 0	

OY 1 TTGAGCTCATCTTCGGG 20
|||||
Db 392 TTGAGCTCATCTTCGGG 411
|||||

RESULT 36
AL606928/c 186605 bp DNA linear ROD 16-FEB-2002
LOCUS Mouse DNA sequence from clone RP23-154F2 on chromosome 3, complete
DEFINITION sequence.
ACCESSION AL606928
VERSION AL606928.9 GI:18655219
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Bukayocia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 186605)
Cordy, N.
Direct Submission
Submitted (16-FEB-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 21, 2002 this sequence version replaced gi:17384520.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em, EMBL; Sw,
SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-154F2 is
from the RPCI-23 Mouse PAC library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pRACE3.6
This sequence is the entire insert of clone RP23-154F2. The true
left end of clone RP23-183J6 is at 140238 in this sequence. The
true right end of clone RP23-212F17 is at 93544 in this sequence.

FEATURES
source
1. 186605
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="3"
/clone="RP23-154F2"
/clone_id="RPCI-23"
4499..4836
/note="Sequence from overlapping clone RP11-212F17
(AL583890). Assembly confirmed by restriction digest."
12403..12687
/note="Sequence from overlapping clone RP11-212F17
(AL583890). Assembly confirmed by restriction digest."
77505
/note="Sequence from overlapping clone RP11-212F17
(AL583890). Assembly confirmed by restriction digest."
95115
/note="Tandem repeat. Forced join. Gap size estimated to
be approximately 40bp by restriction digest data."
183708
/note="Tandem repeat. Forced join. Gap size estimated to

ORIGIN be approximately 110bp by restriction digest data."
Query Match 92.0%; Score 18.4; DB 9; Length 186605;
Best Local Similarity 95.0%; Pred. No. 76;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTGAGCTCATCTTCGGG 20
|||||
Db 181169 TTGAGCTCATCTTCGGG 181150
|||||

RESULT 37
DQ117337/c 399 bp DNA linear ENV 04-SEP-2003
LOCUS Uncultured bacterium clone RS.Muc.107 16S ribosomal RNA gene,
DEFINITION partial sequence.
ACCESSION DQ117337
VERSION DQ117337.1 GI:70672105
KEYWORDS ENV.
SOURCE uncultured bacterium
ORGANISM Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 399)
AUTHORS Kushnaro, A., Ben-Dov, E. and Koopman, N.
TITLE Microbial diversity of Fungia granulosa coral mucus micro-layer
JOURNAL Unpublished
2 (bases 1 to 399)
AUTHORS Kushnaro, A., Ben-Dov, E. and Koopman, N.
TITLE Direct Submission
JOURNAL Submitted (05-JUL-2005) Biotechnology Engineering, Ben Gurion
University, P.O.B. 653, Be'er-Sheva 84105, Israel
Location/Qualifiers
1. 399
/organism="uncultured bacterium"
/mol_type="genomic DNA"
/isolation_source="coral mucus"
/specific_host="Fungia granulosa"
/db_xref="taxon:77133"
/clone="RS.Muc.107"
/environmental_sample
/country="Israel; Red Sea"
<1..>399
/product="16S ribosomal RNA"

ORIGIN
Query Match 90.0%; Score 18; DB 3; Length 399;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 CAGGCTCATCTTCGGG 20
|||||
Db 121 CAGGCTCATCTTCGGG 104
|||||

RESULT 38
AY327227/c 801 bp DNA linear ENV 04-SEP-2003
LOCUS Uncultured bacterium clone ZB35 16S ribosomal RNA gene, partial
DEFINITION sequence.
ACCESSION AY327227
VERSION AY327227.1 GI:32967957
KEYWORDS ENV.
SOURCE uncultured bacterium
ORGANISM Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 801)
AUTHORS Elshahed, M.S., Senko, J.M., Najjar, F.Z., Kenton, S.M., Roe, B.A.,
Dewers, T.A., Spear, J.R. and Krumholz, L.R.
TITLE Bacterial diversity and sulfur cycling in a mesophilic sulfide-rich
spring
JOURNAL Appl. Environ. Microbiol. 69 (9), 5609-5621 (2003)
REFERENCE 2 (bases 1 to 801)

AUTHORS Elishahed,M.S., Senko,J.M., Najaf,F.Z., Kenton,S.M., Roe,B.A.,
Dewers,T.A., Spear,J.R. and Krumholz,L.R.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-2003) Botany and Microbiology, University of
Oklahoma, 770 Van Vleet Oval, Norman, OK 73019, USA
FEATURES
source
1. .801
/organism="uncultured bacterium"
/mol_type="genomic DNA"
/db_xref="taxon:77133"
/clone="ZB35"
/environmental_sample
<1. >801
/product="16S ribosomal RNA"
ORIGIN
Query Match 90.0%; Score 18; DB 3; Length 801;
Best Local Similarity 100.0%; Fred. No. 97;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CAGGCTCATCTCGGTG 20
|||||
230 CAGGCTCATCTCGGTG 213
RESULT 39
AY225134 48352 bp DNA linear VRL 30-JAN-2004
LOCUS Felmannia irregularis virus a strain F1rrv-1 contig B, partial
DEFINITION
ACCESSION AY225134
VERSION AY225134.1 GI:38683699
KEYWORDS
SOURCE
ORGANISM
1. Felmannia irregularis virus a
Felmannia irregularis virus a
viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phaeovirus.
REFERENCE
1 (bases 1 to 48352)
Delaroque,N., Bolland,W., Muller,D.G. and Knipfers,R.
Comparisons of two large phaeoviral genomes and evolutionary
implications
J. Mol. Evol. 57 (6), 613-622 (2003)
1474530
JOURNAL
3 (bases 1 to 48352)
Delaroque,N., Knipfers,R., Mueller,D.G. and Bolland,W.
Partial Nucleotide Sequence of the Felmannia irregularis Virus
F1rrv-1 Genome: On the Evolution of Large Phaeoviral Genomes
Unpublished (2003)
3 (bases 1 to 48352)
Delaroque,N., Knipfers,R., Mueller,D.G. and Bolland,W.
Direct Submission
Submitted (24-JAN-2003) Bioorganics, Max Planck Institute for
Chemical Ecology, Winzerlaer Strasse 10, Jena 07745, Germany
FEATURES
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Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TCAGGCTCATCTTCGGTG 20
DB 36373 TCAGGCTCATCTTCGGTG 36391

RESULT 40
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LOCUS Homo sapiens chromosome 16 clone RP11-465L11, complete sequence.
DEFINITION AC13384
ACCESSION AC13384
VERSION AC13384.1 GI:22380708
KEYWORDS HTG.
ORGANISM Homo sapiens (human)
SOURCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 92474)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratories.
TITLE Direct Submission
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 92474)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Submitted (21-AUG-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
AUTHORS 3 (bases 1 to 92474)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
TITLE Direct Submission
JOURNAL Submitted (24-AUG-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www.hgsc.stanford.edu
Quality: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 0.3.
NOTES: This is not the entire sequence of the clone (entire
sequence is 163,3kb). It is clipped at the overlap with AC091489.
The number of bases overlapped is 56160.

FEATURES
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QY 2 TCAGGCTCATCTTCGGTG 20
DB 30817 TCAGGCTCATCTTCAGTG 30799

Mon Apr 10 07:41:29 2006

us-10-661-094-1_copy_898_917.rge

Page 18

Search completed: April 9, 2006, 07:14:40
Job time : 784.143 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 05:55:33 ; Search time 381.134 Seconds
(without alignments)
472.135 Million cell updates/sec

Title: US-10-661-094-3

Perfect score: 27

Sequence: 1 cctatcctgttttctgtaagccgcgcgc 27

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 333246308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 120 summaries

Database :

N_Geneseq_21:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001as:*
5: geneseq2001bs:*
6: geneseq2002as:*
7: geneseq2002bs:*
8: geneseq2003as:*
9: geneseq2003bs:*
10: geneseq2003cs:*
11: geneseq2003ds:*
12: geneseq2004as:*
13: geneseq2004bs:*
14: geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	27	100.0	1232	4	AAH01063
6	27	100.0	1237	4	AAH01061
7	27	100.0	1241	4	AAH01058
8	27	100.0	1249	4	AAH01059
9	27	100.0	1263	4	AAH01052
10	27	100.0	1265	4	AAH01065
11	27	100.0	1269	4	AAH01066
12	27	100.0	1272	4	AAH01060
13	27	100.0	1768	4	AAH01148
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19	27	100.0	7227	2	AAQ25183

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23	20.8	77.0	110000	2	AAH20248	AAH20248 07
24	20.6	76.3	555	12	ADQ47265	ADQ47265 Enterococ
25	20.6	76.3	556	12	ADQ47264	ADQ47264 Enterococ
26	20.6	76.3	556	12	ADQ47262	ADQ47262 E. faecal
27	20.6	76.3	556	12	ADQ47263	ADQ47263 E. faecal
28	20.6	76.3	556	12	ADQ47261	ADQ47261 E. faecal
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30	20.6	76.3	556	12	ADQ47260	ADQ47260 E. faecal
31	20.6	76.3	556	12	ADQ47259	ADQ47259 E. faecal
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33	20.6	76.3	630	14	ADY59941	ADY59941 Enterococ
34	20.6	76.3	783	14	ADY59942	ADY59942 Enterococ
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37	20.6	76.3	801	14	ADY59940	ADY59940 Enterococ
38	20.6	76.3	801	14	ADY59943	ADY59943 Consensus
39	20.6	76.3	801	14	ADY59936	ADY59936 Enterococ
40	20.6	76.3	801	14	ADY59938	ADY59938 Enterococ
41	20.6	76.3	801	14	ADY59935	ADY59935 Enterococ
42	20.6	76.3	881	12	ADQ47258	ADQ47258 Enterococ
43	20.6	76.3	1029	2	AAV37115	AAV37115 Antibiocl
44	20.6	76.3	1029	4	AAH02303	AAH02303 Enterococ
45	20.6	76.3	1029	4	AAH01720	AAH01720 Enterococ
46	20.6	76.3	1029	4	AAH76048	AAH76048 Enterococ
47	20.6	76.3	1090	14	ADY59931	ADY59931 Enterococ
48	20.6	76.3	1128	10	ADC90583	ADC90583 E. faecium
49	20.6	76.3	1141	2	AAQ69235	AAQ69235 Enterococ
50	20.6	76.3	7160	4	AAH76020	AAH76020 E. faecal
51	20.6	76.3	7678	2	AAH12998	AAH12998 Enterococ
52	20.6	76.3	7678	6	ABH98793	ABH98793 Enterococ
53	19.8	73.3	594	3	AAA8150	AAA8150 D. alamine
54	19.8	73.3	1047	8	ACA48219	ACA48219 Prokaryot
55	19.6	72.6	1191	8	ACA52513	ACA52513 Prokaryot
56	19.6	72.6	21170	2	AAH20535	AAH20535 Polynucle
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61	18.6	68.9	5781	4	AAH76022	AAH76022 E. faecium
62	18.2	67.4	774	5	AAH81838	AAH81838 DNA encod
63	18.2	67.4	819	4	AAH52598	AAH52598 E. coli D
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73	17.8	65.9	772	10	ADH81402	ADH81402 Carboxyl
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83	17.6	65.2	251	12	ADQ06944	ADQ06944 Soybean t
84	17.6	65.2	251	12	ADQ06944	ADQ06944 Soybean t
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93	17.6	65.2	1026	4	AAS53038	AAS53038 Enterococ
94	17.6	65.2	4948	2	AAT42134	AAT42134 ITC-1 gen
95	17.6	65.2	39982	8	AAD48290	AAD48290 Human enz
96	17.6	65.2	66685	4	AAS07380	AAS07380 Human gen
97	17.6	65.2	66686	6	AB573149	AB573149 Human CLA
98	17.4	64.4	318	10	ACF68191	ACF68191 Photorhab
99	17.4	64.4	466	4	AAH34587	AAH34587 Human col
100	17.4	64.4	747	3	AAZ54529	AAZ54529 Neisseria
101	17.4	64.4	754	12	AD062241	AD062241 Transcrip
102	17.4	64.4	1053	11	ABD122733	ABD122733 Pseudom
103	17.4	64.4	1200	13	ADK60608	ADK60608 Plant ful
104	17.4	64.4	1262	12	AD063288	AD063288 Transcrip
105	17.4	64.4	1310	12	AD062242	AD062242 Transcrip
106	17.4	64.4	1353	13	ADK53082	ADK53082 Plant ful
107	17.4	64.4	1512	11	ABD12707	ABD12707 Pseudom
108	17.4	64.4	1865	12	AD062245	AD062245 Transcrip
109	17.4	64.4	2334	11	ABD12689	ABD12689 Pseudom
110	17.4	64.4	3274	2	AAV17622	AAV17622 Plasm sat
111	17.4	64.4	4081	2	AAV06585	AAV06585 Arabidops
112	17.4	64.4	23070	9	ADA02507	ADA02507 Mouse Mnt
113	17.4	64.4	23070	10	ADB72245	ADB72245 Mouse Mnt
114	17.4	64.4	23070	10	ADK57555	ADK57555 Mouse Mnt
115	17.4	64.4	23982	14	ADZ12503	ADZ12503 Murine ca
116	17.4	64.4	73882	13	AD573531	AD573531 tcp gene
117	17.4	64.4	110000	10	ACF67367	ACF67367 Cont. inactio
118	17.4	64.4	110000	10	ACF65384_3	ACF65384_3 Cont. inactio
119	17.4	64.4	111836	13	ABD33102	ABD33102 Murine ca
120	17.4	64.4	256525	11	ACM44148	ACM44148 Mouse gen

ALIGNMENTS

RESULT 1
ADY59929 standard; DNA, 27 BP.

ADY59929;
02-JUN-2005 (first entry)
Enterococcus faecium vana probe SEQ ID NO:3.
DNA detection; antibiotic-resistance; vancomycin; vana; probe; ss.
Enterococcus faecium.
Synthetic.
US2005058985-A1.
17-MAR-2005.
12-SEP-2003; 2003US-00661094.
12-SEP-2003; 2003US-00661094.
(DODG/) DODGSON K J.
Dodgson KJ;
WPI; 2005-222218/23.
Detecting vana and/or vana nucleic acid molecules in a sample, useful for e.g. identifying vancomycin-resistant enterococcus, comprises using vana- and/or vana-specific oligonucleotide probes or primers.
Claim 34; SEQ ID NO 3; 33pp; English.

The invention relates to a method for detecting vancomycin resistance gene vana and/or vana nucleic acid molecules in a sample comprising contacting the sample with a vana- and/or vana-specific oligonucleotide probe or primer, and detecting or determining the presence or amount of hybrid formation or amplified nucleic acid. Also described: (1) an

oligonucleotide composition comprising a first oligonucleotide comprising sequences substantially corresponding to nucleotides 870-896, or an 898-917 of the vana gene, or its complement or portion, or an oligonucleotide comprising sequences substantially corresponding to nucleotides 387-404, 406-423 or 425-446 of the vana gene, or its complement or portion, where the oligonucleotide hybridizes under stringent hybridization conditions to vana or vana DNA; and (2) a kit comprising one or more oligonucleotide(s) specific for a vana gene and/or vana gene in a test sample, comprising the oligonucleotide mentioned above. The method and kit are useful for detecting and/or amplifying genes (i.e. vana and/or vana genes) in a test sample, or for identifying antibiotic resistance genes (e.g. vancomycin-resistant enterococcus). They may also be used in other industrial purposes, such as for quality control of food, water, pharmaceutical products or other products requiring microbiological control. The present sequence represents a probe for Enterococcus faecium vana, which is used in an example from the present invention.

Sequence 27 BP; 3 A; 8 G; 6 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 14; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCCTGTTTGTGTTAAAGCCGCGCC 27
Db 1 CCTATCCCTGTTTGTGTTAAAGCCGCGCC 27

RESULT 2
AAH02300 standard; DNA, 1032 BP.

AAH02300;
24-JUL-2001 (first entry)
Enterococcus faecium nucleotide sequence SEQ ID NO:2293.
Species specific; genus specific; family specific; probe; detection; identification; algal; archaeal; bacterial; fungal; parasiticl;
microorganism; diagnosis; translation elongation factor Tu; toxin;
translation elongation factor G; RecA recombinase; resistance;
catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
primer; ds.
Enterococcus faecium.
WO200123604-A2.
05-APR-2001.
28-SEP-2000; 2000WO-CA001150.
28-SEP-1999; 99CA-02283458.
19-MAY-2000; 2000CA-02307010.
(INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
Bergeon MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
Picard FJ, Roy PH;
WPI; 2001-245006/25.
Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasiticl species in a test sample.
Disclosure; Page 1578; 1580pp; English.

The present invention describes a method for generating a repository of nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic

acids of determined algal, archaeal, bacterial, fungal and parasitica
species with a combination of defined primer pairs. The method can be
used for producing probes and/or primers for detecting one or more
related microorganisms e.g. algae, archaea, bacteria, fungi and
parasites, for universal detection and for specific and ubiquitous
detection and identification of an algal, archaeal, bacterial, fungal and
parasitica species, genus, family and group. A nucleic acid (1) obtained
using the method of the invention can be used for the universal detection
of any bacterium, fungus or parasite in a sample and for the detection of
at least one antimicrobial agent resistance gene or at least one toxin
gene. hexa nucleic acids are used for the specific and ubiquitous
detection and for identification of Streptococcus pneumoniae. (1) can be
used to design a therapeutic agent which is effective against
microorganisms. Microbial species or genus or family or phylum or group
which can be detected include Abiotrophia adiacens, Bordetella sp.,
Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
Mycobacteriaceae family, pseudomonas group, Streptococcus sp., Neisseria
gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
results than substrate specificity tests as results can be determined in
an hour and improved accuracy is also achieved. AAH00010 to AAH002304
represent nucleotide sequences and primers/probes which are given in the
exemplification of the present invention

Sequence 1032 BP; 303 A; 197 C; 264 G; 268 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1032;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCTATCCTGTTTGTAAAGCGGCGC 27
|||||
Db 494 CCTATCCTGTTTGTAAAGCGGCGC 520

RESULT 3

AAAF6039
ID AAFF6039 standard; DNA; 1032 BP.

AAFF6039;

22-MAY-2001 (first entry)

Enterococcus faecium vanA gene, SEQ ID NO:21.

Vancomycin resistance reduction; antisense expression inhibition;
competitive inducer sequestration; van promoter; van gene product;
Enterococcus; Staphylococcus; Streptococcus; Gram-positive bacterium;
antibiotic susceptibility; ex vivo eradication; in vivo eradication;
glycopeptide resistance; VanA gene cluster; ds.

Enterococcus faecium.

WO200112803-A2.

22-FEB-2001.

11-AUG-2000; 2000WO-US022086.

17-AUG-1999; 99US-0149313P.

(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

Inouye RT, Torres-Viera C, Moellering R, Gold H, Eliopoulos GM;

WPI; 2001-211216/21.

Reducing vancomycin-resistance in vancomycin-resistant organism by
introducing a antisense vancomycin-resistance molecule to inhibit
vancomycin-resistance gene expression, or by enhancing van promoter
expression.

Example; Page 52; 59pp; English.

The invention relates to methods of reducing vancomycin resistance in a
vancomycin-resistant organism. One method involves introducing a
vancomycin resistance gene antisense nucleic acid into the organism;
antisense oligonucleotides complementary to AAFF603-AAFF6031 are
particularly preferred for this purpose. The second method involves
providing additional van promoter sequences which are not operatively
coupled to a vancomycin resistance gene, so that the phosphorylated van
gene product (which induces van promoter activity) is competitively
sequestered. Both methods are able to restore antibiotic susceptibility
in glycopeptide resistant enterococci. The methods of the invention are
useful for reducing vancomycin resistance in a vancomycin resistant
organism, particularly Enterococcus faecium and Enterococcus faecalis,
but also in other Gram-positive bacteria such as Staphylococcus sp. and
Corynebacterium sp., to which Enterococcus faecium and Enterococcus
faecalis have the potential to transfer resistance determinants. The
antisense molecules are useful in the treatment of infection and
colonisation by vancomycin resistant enterococci and other clinically
significant pathogens, and may be used for the ex vivo eradication of
vancomycin-resistant enterococci from frequently colonised settings, such
as intensive care units, haemodialysis units, and chronic care facilities
; for the in vivo clearance of vancomycin-resistant enterococci from
colonised gastrointestinal or genitourinary tracts of animals, including
humans; and in primary or adjuvant therapy for vancomycin-resistant
enterococcal infections. The gene based strategy targets key vancomycin
resistance determinants and results in restoration of vancomycin
susceptibility in previously glycopeptide-resistant enterococci.
Sequences AAFF603-AAFF6042 represent genes of the Enterococcus faecium
VanA gene cluster

Sequence 1032 BP; 303 A; 197 C; 264 G; 268 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1032;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCTATCCTGTTTGTAAAGCGGCGC 27
|||||
Db 494 CCTATCCTGTTTGTAAAGCGGCGC 520

RESULT 4

AAH01064
ID AAH01064 standard; DNA; 1218 BP.

AAH01064;

24-JUL-2001 (first entry)

Enterococcus gallinarum nucleotide sequence SEQ ID NO:1055.

Species specific; genus specific; family specific; probe; detection;
identification; algal; archaeal; bacterial; fungal; parasitica;
microorganism; diagnosis; translation elongation factor Tu; toxin;
translation elongation factor G; RecA recombinase; resistance;
catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
primer; ds.

Enterococcus gallinarum.

WO200123604-A2.

05-APR-2001.

28-SEP-2000; 2000WO-CA001150.

28-SEP-1999; 99CA-02283458.

19-MAY-2000; 2000CA-02307010.

(INFB-) INFECTIO DIAGNOSTIC (IDI) INC.

Bergeron MG, Bolesnot M, Huletsky A, Menard C, Ouellette M;
Picard FJ, Roy PH;

DR WPI, 2001-245006/25.

XX Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitological species in a test sample.

PS Claim 27, Page 1001-1002; 1580pp; English.

XX The present invention describes a method for generating a repository of
CC nucleic acids of ruf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitological
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitological species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention

SQ Sequence 1218 BP; 364 A; 226 C; 311 G; 317 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1218;

Best Local Similarity 100.0%; Pred. No. 0.031;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGATCCTGTTTGTAAAGCCGCGC 27

DB 568 CCGATCCTGTTTGTAAAGCCGCGC 594

RESULT 5

AAH01063 ID AAH01063 standard; DNA; 1232 BP.

XX AAH01063;

DT 24-JUL-2001 (first entry)

DE Enterococcus faecalis nucleotide sequence SEQ ID NO:1054.

XX Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitological;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.

OS Enterococcus faecalis.

XX WO200123604-A2.

XX 05-APR-2001.

XX 28-SEP-2000; 2000WO-CA001150.

XX 28-SEP-1999; 99CA-02283458.

XX 19-MAY-2000; 2000CA-02307010.

PA (INFR-) INFECTIO DIAGNOSTIC (IDI) INC.

XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;

XX WPI, 2001-245006/25.

XX Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitological species in a test sample.

PS Claim 27, Page 1001; 1580pp; English.

XX The present invention describes a method for generating a repository of
CC nucleic acids of ruf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitological
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitological species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention

SQ Sequence 1232 BP; 367 A; 228 C; 313 G; 323 T; 0 U; 1 Other;

Query Match 100.0%; Score 27; DB 4; Length 1232;

Best Local Similarity 100.0%; Pred. No. 0.031;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGATCCTGTTTGTAAAGCCGCGC 27

DB 578 CCGATCCTGTTTGTAAAGCCGCGC 604

RESULT 6

AAH01061 ID AAH01061 standard; DNA; 1237 BP.

XX AAH01061;

DT 24-JUL-2001 (first entry)

DE Enterococcus faecium nucleotide sequence SEQ ID NO:1052.

XX Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitological;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.

OS Enterococcus faecium.

XX WO200123604-A2.

XX 05-APR-2001.

PF 28-SEP-2000; 2000MO-CA001150.
 XX 28-SEP-1999; 99CA-02283458.
 FR 19-MAY-2000; 2000CA-02307010.
 XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
 XX Bergerson MG, Bolssinot M, Huletsky A, Menard C, Ouellette M;
 PI Picard FJ, Roy PH;
 XX WPI; 2001-245006/25.
 DR Nucleic acid sequences are used to generate universal probes and primers
 PT which can be used to identify and detect the presence of algal, archaeal,
 PT bacterial, fungal and parasitological species in a test sample.
 XX
 XX Claim 27; Page 999; 1580pp; English.
 PS The present invention describes a method for generating a repertoire of
 CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
 CC and/or primers are derived. The method comprises amplifying the nucleic
 CC acids of determined algal, archaeal, bacterial, fungal and parasitological
 CC species with a combination of defined primer pairs. The method can be
 CC used for producing probes and/or primers for detecting one or more
 CC related microorganisms e.g. algae, archaea, bacteria, fungi and
 CC parasites, for universal detection and for specific and ubiquitous
 CC detection and identification of an algal, archaeal, bacterial, fungal and
 CC parasitological species, genus, family and group. A nucleic acid (I) obtained
 CC using the method of the invention can be used for the universal detection
 CC of any bacterium, fungus or parasite in a sample and for the detection of
 CC at least one antimicrobial agent resistance gene or at least one toxin
 CC gene. hexA nucleic acids are used for the specific and ubiquitous
 CC detection and for identification of Streptococcus pneumoniae. (I) can be
 CC used to design a therapeutic agent which is effective against
 CC microorganisms. Microbial species or genus or family or phylum or group
 CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
 CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
 CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
 CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
 CC results than substrate specificity tests as results can be determined in
 CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
 CC represent nucleotide sequences and primers/probes which are given in the
 CC exemplification of the present invention
 CC
 CC Sequence 1237 BP; 366 A; 235 C; 314 G; 322 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 27; DB 4; Length 1237;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTATCCTGTTTGTTAAGCGGCGC 27
 DB 590 CCTATCCTGTTTGTTAAGCGGCGC 616
 RESULT 7
 ID AAH01058 standard; DNA; 1241 BP.
 XX AAH01058;
 XX 24-JUL-2001 (first entry)
 DE Enterococcus faecium nucleotide sequence SEQ ID NO:1049.
 XX Species specific; genus specific; family specific; probe; detection;
 XX identification; algal; archaeal; bacterial; fungal; parasitological;
 XX microorganism; diagnosis; translation elongation factor Tu; toxin;
 XX translation elongation factor G; RecA recombinase; resistance;
 XX catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
 XX primer; ds.
 XX Enterococcus faecium.
 OS

XX W0200123604-A2.
 PN 05-APR-2001.
 XX 28-SEP-2000; 2000MO-CA001150.
 XX 28-SEP-1999; 99CA-02283458.
 PR 19-MAY-2000; 2000CA-02307010.
 XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
 XX Bergerson MG, Bolssinot M, Huletsky A, Menard C, Ouellette M;
 PI Picard FJ, Roy PH;
 XX WPI; 2001-245006/25.
 DR Nucleic acid sequences are used to generate universal probes and primers
 PT which can be used to identify and detect the presence of algal, archaeal,
 PT bacterial, fungal and parasitological species in a test sample.
 XX
 XX Claim 27; Page 997; 1580pp; English.
 PS The present invention describes a method for generating a repertoire of
 CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
 CC and/or primers are derived. The method comprises amplifying the nucleic
 CC acids of determined algal, archaeal, bacterial, fungal and parasitological
 CC species with a combination of defined primer pairs. The method can be
 CC used for producing probes and/or primers for detecting one or more
 CC related microorganisms e.g. algae, archaea, bacteria, fungi and
 CC parasites, for universal detection and for specific and ubiquitous
 CC detection and identification of an algal, archaeal, bacterial, fungal and
 CC parasitological species, genus, family and group. A nucleic acid (I) obtained
 CC using the method of the invention can be used for the universal detection
 CC of any bacterium, fungus or parasite in a sample and for the detection of
 CC at least one antimicrobial agent resistance gene or at least one toxin
 CC gene. hexA nucleic acids are used for the specific and ubiquitous
 CC detection and for identification of Streptococcus pneumoniae. (I) can be
 CC used to design a therapeutic agent which is effective against
 CC microorganisms. Microbial species or genus or family or phylum or group
 CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
 CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
 CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
 CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
 CC results than substrate specificity tests as results can be determined in
 CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
 CC represent nucleotide sequences and primers/probes which are given in the
 CC exemplification of the present invention
 CC
 CC Sequence 1241 BP; 371 A; 228 C; 317 G; 325 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 27; DB 4; Length 1241;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTATCCTGTTTGTTAAGCGGCGC 27
 DB 561 CCTATCCTGTTTGTTAAGCGGCGC 587
 RESULT 8
 ID AAH01059 standard; DNA; 1249 BP.
 XX AAH01059;
 XX 24-JUL-2001 (first entry)
 DE Enterococcus gallinarum nucleotide sequence SEQ ID NO:1050.
 XX Species specific; genus specific; family specific; probe; detection;
 XX identification; algal; archaeal; bacterial; fungal; parasitological;
 XX microorganism; diagnosis; translation elongation factor Tu; toxin;
 XX

KM translation elongation factor G; RecA recombinase; resistance;
 KM catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
 KM primer; ds.
 XX
 OS Enterococcus gallinarum.
 XX
 PN W0200123604-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 28-SEP-2000; 2000MO-CA001150.
 XX
 PR 28-SEP-1999; 99CA-02283458.
 PR 19-MAY-2000; 2000CA-02307010.
 XX
 PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
 XX
 PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
 PI Picard FJ, Roy PH;
 XX
 DR WPI; 2001-245006/25.
 XX
 PT Nucleic acid sequences are used to generate universal probes and primers
 PT which can be used to identify and detect the presence of algal, archaeal,
 PT bacterial, fungal and parasitcal species in a test sample.
 XX
 PS Claim 27; Page 998; 1580pp; English.
 XX
 CC The present invention describes a method for generating a repertory of
 CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
 CC and/or primers are derived. The method comprises amplifying the nucleic
 CC acids of determined algal, archaeal, bacterial, fungal and parasitcal
 CC species with a combination of defined primer pairs. The method can be
 CC used for producing probes and/or primers for detecting one or more
 CC related microorganisms e.g. algae, archaea, bacteria, fungi and
 CC parasites, for universal detection and for specific and ubiquitous
 CC detection and for identification of an algal, archaeal, bacterial, fungal and
 CC parasitcal species, genus, family and group. A nucleic acid (I) obtained
 CC using the method of the invention can be used for the universal detection
 CC of any bacterium, fungus or parasite in a sample and for the detection of
 CC at least one antimicrobial agent resistance gene or at least one toxin
 CC gene. hexA nucleic acids are used for the specific and ubiquitous
 CC detection and for identification of Streptococcus pneumoniae. (I) can be
 CC used to design a therapeutic agent which is effective against
 CC microorganisms. Microbial species or genus or family or phylum or group
 CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
 CC Corynebacterium sp., Enterobacteriaceae group, Baccharichia coli,
 CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
 CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
 CC results than substrate specificity tests as results can be determined in
 CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
 CC represent nucleotide sequences and primers/probes which are given in the
 CC exemplification of the present invention
 XX
 SQ Sequence 1249 BP; 373 A; 235 C; 316 G; 325 T; 0 U; 0 Other;
 XX
 QY Query Match 100.0%; Score 27; DB 4; Length 1249;
 Db Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CCTATCCTGTTTGTGTTAAGCCGCGC 27
 590 CCTATCCTGTTTGTGTTAAGCCGCGC 616
 RESULT 9
 AAH01062
 ID AAH01062 standard; DNA; 1263 BP.
 XX
 AC AAH01062;
 XX
 DT 24-JUL-2001 (first entry)
 XX

DE Enterococcus faecium nucleotide sequence SEQ ID NO:1053.
 XX
 XX Species specific; genus specific; family specific; probe; detection;
 KM identification; algal; archaeal; bacterial; fungal; parasitcal;
 KM microorganism; diagnosis; translation elongation factor Tu; toxin;
 KM translation elongation factor G; RecA recombinase; resistance;
 KM catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
 KM primer; ds.
 XX
 OS Enterococcus faecium.
 XX
 PN W0200123604-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 28-SEP-2000; 2000MO-CA001150.
 XX
 PR 28-SEP-1999; 99CA-02283458.
 PR 19-MAY-2000; 2000CA-02307010.
 XX
 PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
 XX
 PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
 PI Picard FJ, Roy PH;
 XX
 DR WPI; 2001-245006/25.
 XX
 PT Nucleic acid sequences are used to generate universal probes and primers
 PT which can be used to identify and detect the presence of algal, archaeal,
 PT bacterial, fungal and parasitcal species in a test sample.
 XX
 PS Claim 27; Page 1000; 1580pp; English.
 XX
 CC The present invention describes a method for generating a repertory of
 CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
 CC and/or primers are derived. The method comprises amplifying the nucleic
 CC acids of determined algal, archaeal, bacterial, fungal and parasitcal
 CC species with a combination of defined primer pairs. The method can be
 CC used for producing probes and/or primers for detecting one or more
 CC related microorganisms e.g. algae, archaea, bacteria, fungi and
 CC parasites, for universal detection and for specific and ubiquitous
 CC detection and for identification of an algal, archaeal, bacterial, fungal and
 CC parasitcal species, genus, family and group. A nucleic acid (I) obtained
 CC using the method of the invention can be used for the universal detection
 CC of any bacterium, fungus or parasite in a sample and for the detection of
 CC at least one antimicrobial agent resistance gene or at least one toxin
 CC gene. hexA nucleic acids are used for the specific and ubiquitous
 CC detection and for identification of Streptococcus pneumoniae. (I) can be
 CC used to design a therapeutic agent which is effective against
 CC microorganisms. Microbial species or genus or family or phylum or group
 CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
 CC Corynebacterium sp., Enterobacteriaceae group, Baccharichia coli,
 CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
 CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
 CC results than substrate specificity tests as results can be determined in
 CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
 CC represent nucleotide sequences and primers/probes which are given in the
 CC exemplification of the present invention
 XX
 SQ Sequence 1263 BP; 378 A; 234 C; 321 G; 330 T; 0 U; 0 Other;
 XX
 QY Query Match 100.0%; Score 27; DB 4; Length 1263;
 Db Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CCTATCCTGTTTGTGTTAAGCCGCGC 27
 582 CCTATCCTGTTTGTGTTAAGCCGCGC 608
 RESULT 10
 AAH01065
 ID AAH01065 standard; DNA; 1265 BP.
 XX

XX
AC AAH01065;
XX
DT 24-JUL-2001 (first entry)
XX
DE Enterococcus faecium nucleotide sequence SEQ ID NO:1056.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitical;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
XX
OS Enterococcus faecium.
XX
XX MO200123604-A2.
XX
PN 05-APR-2001.
XX
PD 28-SEP-2000; 2000MO-CA001150.
XX
PF 28-SEP-1999; 99CA-02283458.
XX
PR 19-MAY-2000; 2000CA-02307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
DR WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
PS Claim 27; Page 1002; 1580pp; English.
XX
CC The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention.
XX
SQ Sequence 1265 BP; 379 A; 237 C; 320 G; 329 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1265;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCGATCCGTTTGTGTAAGCCGCGC 27
|||||
592 CCGATCCGTTTGTGTAAGCCGCGC 618

RESULT 11
ID AAH01066
XX
AC AAH01066;
XX
DT 24-JUL-2001 (first entry)
XX
DE Enterococcus faecium nucleotide sequence SEQ ID NO:1057.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitical;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
XX
OS Enterococcus faecium.
XX
XX MO200123604-A2.
XX
PN 05-APR-2001.
XX
PD 28-SEP-2000; 2000MO-CA001150.
XX
PF 28-SEP-1999; 99CA-02283458.
XX
PR 19-MAY-2000; 2000CA-02307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
DR WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
PS Claim 27; Page 1003; 1580pp; English.
XX
CC The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 1269 BP; 380 A; 238 C; 321 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1269;
Best Local Similarity 100.0%; Pred. No. 0.031;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCTATCCTGTTTGTAAAGCCGCGC 27
Db 590 CCTATCCTGTTTGTAAAGCCGCGC 616

RESULT 12
AAH01060
ID AAH01060 standard; DNA; 1272 BP.

XX AAH01060;

XX 24-JUL-2001 (first entry)

DE Enterococcus faecium nucleotide sequence SEQ ID NO:1051.

XX Species specific; genus specific; family specific; probe; detection;
XX identification; algal; archaeal; bacterial; fungal; parasitcal;
XX microorganism; diagnosis; translation elongation factor Tu; toxin;
XX translation elongation factor G; RecA recombinase; resistance;
XX catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
XX primer; de.

OS Enterococcus faecium.

XX MO200123604-A2.

XX 05-APR-2001.

XX 28-SEP-2000; 2000MO-CA001150.

XX 28-SEP-1999; 99CA-02283458.

PR 19-MAY-2000; 2000CA-02307010.

XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;

PI Picard FJ, Roy PH;

XX WPI; 2001-24506/25.

XX Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
XX bacterial, fungal and parasitcal species in a test sample.

PS Claim 27; Page 998-999; 1580pp; English.

XX The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitcal
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitcal species; genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention

XX SQ Sequence 1272 BP; 379 A; 232 C; 325 G; 336 T; 0 U; 0 Other;
Query Match 100.0%; Score 27; DB 4; Length 1272;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTAAAGCCGCGC 27
Db 570 CCTATCCTGTTTGTAAAGCCGCGC 596

RESULT 13
AAH01148
ID AAH01148 standard; DNA; 1768 BP.

XX AAH01148;

XX 24-JUL-2001 (first entry)

DE Enterococcus faecium nucleotide sequence SEQ ID NO:1139.

XX Species specific; genus specific; family specific; probe; detection;
XX identification; algal; archaeal; bacterial; fungal; parasitcal;
XX microorganism; diagnosis; translation elongation factor Tu; toxin;
XX translation elongation factor G; RecA recombinase; resistance;
XX catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
XX primer; de.

OS Enterococcus faecium.

XX MO200123604-A2.

XX 05-APR-2001.

XX 28-SEP-2000; 2000MO-CA001150.

XX 28-SEP-1999; 99CA-02283458.

PR 19-MAY-2000; 2000CA-02307010.

XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;

PI Picard FJ, Roy PH;

XX WPI; 2001-24506/25.

XX Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
XX bacterial, fungal and parasitcal species in a test sample.

PS Disclosure; Page 1033-1034; 1580pp; English.

XX The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitcal
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitcal species; genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria

gonorrhoeae and *Staphylococcus* sp. . Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AAH0010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention

Sequence 1768 BP; 537 A; 336 C; 437 G; 458 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1768;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCTATCCTGTTTGTGTTAGCCGCGC 27
870 CCTATCCTGTTTGTGTTAGCCGCGC 896

RESULT 14

ADO47257 standard; DNA; 1768 BP.

ADO47257;

15-JUL-2004 (first entry)

E. faecium vancomycin resistance gene, *vanA*.

Vancomycin resistant enterococcus; vancomycin resistance gene; *vanA*;

gene; ds; hospital acquired infection; VRB;

fluorescence resonance energy transfer; FRRT.

Enterococcus faecium.

US2004058336-A1.

25-MAR-2004.

25-SEP-2002; 2002US-00254260.

25-SEP-2002; 2002US-00254260.

(COCK/) COCKERILL F R.

(SLOAN/) SLOAN L M.

Cockerill FR, Sloan LM;

WPI; 2004-268785/25.

Detecting presence or absence of vancomycin-resistant enterococci in biological sample from individual comprises using real time polymerase chain reaction.

disclosure; SEQ ID NO 10; 33pp; English.

The invention relates to detecting the presence or absence of vancomycin-resistant enterococci (VRB) in a sample, comprising performing a cycling step by amplifying a sample with pair of *vanA* or *vanB* primers and hybridizing the sample with a pair of *vanA* or *vanB* probes, labelled with donor and acceptor fluorescent group, respectively, detecting fluorescence resonance energy transfer (FRET), where the presence of FRET indicates presence of VRB. Also included is an article of manufacture, comprising a pair of *vanA* or *vanB* primers, a pair of *vanA* or *vanB* probes and a donor fluorescent group and a corresponding fluorescent group. The method is useful for detecting the presence or absence of vancomycin-resistant enterococci in a biological sample, e.g. stool samples, anal or perirectal swabs, blood and body fluids from an individual. The method replaces standard culture methods and reduces the cost. The method provides rapid vancomycin resistant enterococcus real time PCR assay which is useful for beginning the antimicrobial therapy immediately to treat hospital acquired infection. The present sequence is an enterococcal *vanA*, vancomycin resistance gene.

Sequence 1768 BP; 537 A; 336 C; 437 G; 458 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 12; Length 1768;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCTATCCTGTTTGTGTTAGCCGCGC 27
870 CCTATCCTGTTTGTGTTAGCCGCGC 896

RESULT 15

ADY5927 standard; DNA; 1768 BP.

ADY5927;

02-JUN-2005 (first entry)

Enterococcus faecium *vanA* DNA sequence SEQ ID NO:1.

DNA detection; antibiotic-resistance; vancomycin; *vanA*; gene; ds.

Enterococcus faecium.

US2005058985-A1.

17-MAR-2005.

12-SEP-2003; 2003US-00661094.

12-SEP-2003; 2003US-00661094.

(DODG/) DODGSON K J.

Dodgson KJ;

WPI; 2005-222218/23.

Detecting *vanA* and/or *vanB* nucleic acid molecules in a sample, useful for e.g. identifying vancomycin-resistant enterococcus, comprises using *vanA*- and/or *vanB*-specific oligonucleotide probes or primers.

Example 1; SEQ ID NO 1; 33pp; English.

The invention relates to a method for detecting vancomycin resistance gene *vanA* and/or *vanB* nucleic acid molecules in a sample comprising contacting the sample with a *vanA*- and/or *vanB*-specific oligonucleotide probe or primer, and detecting or determining the presence or amount of hybrid formation or amplified nucleic acid. Also described: (1) an oligonucleotide composition comprising a first oligonucleotide comprising sequences substantially corresponding to nucleotides 870-896, 851-868 or 898-917 of the *vanA* gene, or its complement or portion, or an oligonucleotide comprising sequences substantially corresponding to nucleotides 387-404, 406-423 or 426-446 of the *vanB* gene, or its complement or portion, where the oligonucleotide hybridizes under stringent hybridization conditions to *vanA* or *vanB* DNA; and (2) a kit comprising one or more oligonucleotide(s) specific for a *vanA* gene and/or *vanB* gene in a test sample, comprising the oligonucleotide mentioned above. The method and kit are useful for detecting and/or amplifying genes (i.e. *vanA* and/or *vanB* genes) in a test sample, or for identifying antibiotic resistance genes (e.g. vancomycin-resistant enterococcus). They may also be used in other industrial purposes, such as for quality control of food, water, pharmaceutical products or other products requiring microbiological control. The present sequence represents an Enterococcus faecium *vanA* nucleotide sequence from the present invention.

Sequence 1768 BP; 537 A; 336 C; 437 G; 458 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 14; Length 1768;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCTATCCTGTTTGTGTTAGCCGCGC 27

Db 870 CCTATCCTGTTTGTAAAGCCGCCG 896

RESULT 16

AA728569 standard; DNA; 2607 BP.

AA728569;

01-APR-1997 (first entry)

Bacterial antibiotic resistance gene, vanH, vanA and vanX, probe.

Detection; probe: amplification primer; bacterial pathogen; pneumonia; *Escherichia coli*; *Klebsiella pneumoniae*; *Pseudomonas aeruginosa*; *Streptococcus pneumoniae*; *Staphylococcus aureus*; *Staphylococcus epidermidis*; *Enterococcus faecalis*; respiratory tract; *Staphylococcus saprophyticus*; *Streptococcus pyogenes*; urinary tract; *Haemophilus influenzae*; *Moraxella catarrhalis*; septicemia; meningitis; infection; intra-abdominal infection; skin infection; bacterial resistance; beta-lactam antibiotic; ds.

Synthetic.

MO9608582-A2.

21-MAR-1996.

12-SEP-1995; 95WO-CA000528.

12-SEP-1994; 94US-00304732.

(BERG/) BERGERON M. G.

(OUEL/) OUELLETTE M.

(ROY/) ROY P. H.

Bergeron MG, Ouellette M, Roy PH;

WPI; 1996-179953/18.

Method for the detection of bacterial species using probes and primers - allows detection and quantification of antibiotic resistant bacteria in patients, the environment and food.

Claim 94; Page 145-147; 216pp; English.

The sequences given in AA728560-76 represent fragments derived from bacterial antibiotic resistance genes which were used as probes in the method of the invention for the detection of bacterial species in a sample. The method of the invention comprises using probes and/or amplification primers which are specific, ubiquitous and sensitive for determining the presence and/or amount of nucleic acids from selected bacterial species in any sample, where the bacterial nucleic acid comprises a selected target region hybridisable with the probes or primers. The method comprises contacting the sample with the probes or primers and detecting the presence and/or amount of hybridised primers or amplification products as and indication of the presence and/or amount of the bacterial species. This method may be used to detect commonly encountered bacterial pathogens, e.g. *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Proteus mirabilis*, *Streptococcus pneumoniae*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Enterococcus faecalis*, *Staphylococcus saprophyticus*, *Streptococcus pyogenes*, *Haemophilus influenzae* and *Moraxella catarrhalis*. These bacterial species are associated with approx. 90% of urinary tract infections and with a high percentage of other severe infections including septicemia, meningitis, pneumonia, intra-abdominal infections, skin infections and other severe respiratory tract infections. The method may also be used to evaluate a bacterial resistance to beta-lactam antibiotics

Sequence 2607 BP; 768 A; 506 C; 652 G; 681 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 2; Length 2607;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCTATCCTGTTTGTAAAGCCGCCG 27

Db 1455 CCTATCCTGTTTGTAAAGCCGCCG 1481

RESULT 17

ABA76994 standard; DNA; 2607 BP.

ABA76994;

28-JAN-2002 (first entry)

Antibiotic resistance detection polynucleotide SEQ ID NO 170.

Detection; bacterial species; animal; food; environment; antibiotic resistance; ds.

Undenified.

NZ501596-A.

29-JUN-2001.

12-SEP-1995; 95NZ-00501596.

12-SEP-1995; 95NZ-00501596.

(IDI-) IDI INFECTIO DIAGNOSTIC INC.

Bergeron MG, Ouellette M, Roy PH;

WPI; 2001-615034/71.

Method for detecting target bacterial species in a sample, comprises detecting the presence or amount of bacterial nucleic acid amplified by a primer derived from bacterial DNA, specific for the target bacterial species.

Claim 16; Page 160-162; 168pp; English.

The invention relates to detecting target bacterial species suspected to be present in a sample, comprising contacting nucleic acids of target bacterial species with an amplification primer pair derived from a bacterial DNA fragment (ABA76825-ABA76861) specific for the target bacterial species but ubiquitous for different strains, amplifying the nucleic acid and detecting the presence or amount of an amplified sequence as an indication of the presence or amount of the target bacterial species. The invention includes primers and probes (ABA76862-ABA76984) against the target bacterial species, especially *E. coli*, *K. pneumoniae*, *P. aeruginosa*, *P. mirabilis*, *S. pneumoniae*, *S. aureus*, *M. catarrhalis* and/or group A *Streptococci* producing exotoxin A gene *spe A*, suspected to be present in a sample which is obtained from human patients, animals, environment or food, and which consists of one or more bacterial colonies. Oligonucleotide probes and primers complementary to the bacterial genes encoding resistance to antibiotics such as bla(tem), bla(rob), bla(shv), aadB, aacC1, aacC2, aacC3, aacA4, meca, vanA, vanH, vanX, aacA, aacA-phd, vat, vga, mcrA, sul and/or int (ABA76985-ABA77001) are also useful to identify commonly encountered and clinically important resistance genes. The invention provides a rapid method of bacterial identification that can be achieved, which reduces the time currently required for the identification of pathogens in the clinical laboratory

Sequence 2607 BP; 768 A; 506 C; 652 G; 681 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 2607;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTAAAGCGGCGC 27
DB 1455 CCTATCCTGTTTGTAAAGCGGCGC 1481

RESULT 18

ID AAH01150 standard; DNA; 3946 BP.

AC AAH01150;

DT 24-JUL-2001 (first entry)

DE Enterococcus faecium nucleotide sequence. SEQ ID NO:1141.

XX Species specific; genus specific; family specific; probe; detection;
XX Identification; algal; archaeal; bacterial; fungal; parasiticol;
XX microorganism; diagnosis; translation elongation factor Tu; toxin;
XX translation elongation factor G; RecA recombinase; resistance;
XX catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
XX primer; ds.

OS Enterococcus faecium.

PN W0200123604-A2.

PD 05-APR-2001.

PF 28-SBP-2000; 2000WO-CA001150.

PR 28-SBP-1999; 99CA-02283458.

PR 19-MAY-2000; 2000CA-02307010.

PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;

XX WPI; 2001-245006/25.

PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasiticol species in a test sample.

PS Disclosure; Page 1035-1036; 1580pp; English.

XX The present invention describes a method for generating a repository of
XX nucleic acids of tuf, fus, atpD and/or recA genes from which probes
XX and/or primers are derived. The method comprises amplifying the nucleic
XX acids of determined algal, archaeal, bacterial, fungal and parasiticol
XX species with a combination of defined primer pairs. The method can be
XX used for producing probes and/or primers for detecting one or more
XX related microorganisms e.g. algae, archaea, bacteria, fungi and
XX parasites, for universal detection and for specific and ubiquitous
XX parasiticol and identification of an algal, archaeal, bacterial, fungal and
XX parasiticol species, genus, family and group. A nucleic acid (I) obtained
XX using the method of the invention can be used for the universal detection
XX of any bacterium, fungus or parasite in a sample and for the detection of
XX at least one antimicrobial agent resistance gene or at least one toxin
XX gene. hexA nucleic acids are used for the specific and ubiquitous
XX detection and for identification of Streptococcus pneumoniae. (I) can be
XX used to design a therapeutic agent which is effective against
XX microorganisms. Microbial species or genus or family or phylum or group
XX which can be detected include Abiotrophia adiacens, Bordetella sp.,
XX Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
XX Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
XX gonorrhoeae and Streptococcus sp.. Using DNA based tests provides faster
XX results than substrate specificity tests as results can be determined in
XX an hour and improved accuracy is also achieved. AAH00010 to AAH002304
XX represent nucleotide sequences and primers/probes which are given in the
XX exemplification of the present invention

SQ Sequence 3946 BP; 1235 A; 706 C; 936 G; 1069 T; 0 U; 0 Other;
Query Match 100.0%; Score 27; DB 4; Length 3946;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTAAAGCGGCGC 27

DB 1455 CCTATCCTGTTTGTAAAGCGGCGC 1481

RESULT 19

ID AAQ25183 standard; DNA; 7227 BP.

AC AAQ25183;

DT 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 20-NOV-1992 (first entry)

DE E. faecium antibiotic resistance genes and flanking sequences.

XX Glycopeptide antibiotic; Vancomycin; telicoplanin; resistant;
XX D-Ala-D-Ala ligase; peptidoglycan precursor; transposon;
XX inverted repeats; vanR; vanS; vanH; vanA; vanX; sb.

OS Enterococcus faecium; BM4147.

PN W09207942-A1.

PD 14-MAY-1992.

PF 29-OCT-1991; 91WO-FR000855.

PR 31-OCT-1990; 90FR-00013579.

PA (INSP) INST PASTEUR.

PI Arthur M, Dukt-Malen S, Molinas C, Courvillain P;

DR WPI; 1992-183677/22.

DR P-PSDB; AAR24305, AAR24306, AAR24307.

PT Polypeptides involved in expression of glycopeptide antibiotic resistance
PT - useful in diagnosing presence of Gram-positive enterococcal strains
PT e.g. Enterococcus faecium and E. Gallinarum.

PS Disclosure; Fig 4; 163pp; French.

XX This sequence contains the genes vanH, vanA, vanX, vanR and vanS. The
XX proteins encoded by the latter two genes (i.e. proteins vanR and vanS)
XX have a regulatory function and control expression of the other three
XX ("protective") proteins. See also AAQ25179-025182. (Updated on 25-MAR-
XX 2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)
XX (Updated on 24-OCT-2003 to standardise OS field)

SQ Sequence 7227 BP; 2313 A; 1305 C; 1596 G; 2011 T; 0 U; 2 Other;

Query Match 100.0%; Score 27; DB 2; Length 7227;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTAAAGCGGCGC 27

DB 5018 CCTATCCTGTTTGTAAAGCGGCGC 5044

RESULT 20

ID AAQ25178 standard; DNA; 10851 BP.

AC AAQ25178;

XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 20-NOV-1992 (first entry)
XX E. faecium antibiotic resistance genes and Tn sequences.
XX glycopeptide antibiotic; vancomycin; telicoplanin; resistant;
KM D-Ala-D-Ala ligase; peptidoglycan precursor; transposon;
KM inverted repeats; ss.
XX Enterococcus faecium; BM4147.
XX location/Qualifiers
FH Key complement (1. .3189)
FH CDS /tag= a
FT /product= "transposase"
FT /note= "coded by the (-) strand - see AAQ25179"
FT repeat_unit
FT 1. .38
FT /tag= j
FT /rpt_type= INVERTED
FT CDS 3187. .3762
FT /tag= b
FT /product= "resolvase"
FT 3976. .4671
FT /tag= c
FT /product= "VanR"
FT /note= "VanR is a transcription activator"
FT CDS 4649. .5803
FT /tag= d
FT /product= "Vans"
FT /note= "Vans is a regulatory protein"
FT CDS 6018. .6986
FT /tag= e
FT /product= "VanH"
FT 6979. .8010
FT /tag= f
FT /product= "VanA"
FT CDS 8016. .8624
FT /tag= g
FT /product= "VanX"
FT 9052. .9963
FT /tag= h
FT /product= "Vany"
FT CDS 10116. .10601
FT /tag= i
FT /product= "VanZ"
FT repeat_unit
FT complement (10814. .10851)
FT /tag= k
FT /rpt_type= INVERTED
XX WO9207942-A1.
XX 14-MAY-1992.
XX 29-OCT-1991; 91WO-FR000855.
XX 31-OCT-1990; 90FR-00013579.
XX (INSP) INST PASTEUR.
XX Arthur M, Dutka-Malen S, Molinas C, Courvalin P,
XX WPI; 1992-183677/22.
XX P-PSDB; AAR24294, AAR24295, AAR24296, AAR24297, AAR24298, AAR24299,
XX AAR24300, AAR24301, AAR24302.
XX Polypeptides involved in expression of glycopeptide antibiotic resistance
PT - useful in diagnosing presence of Gram-positive enterococcal strains
PT e.g. Enterococcus faecium and B Gallinarum.
XX Claim 9; Fig 8; 163pp; French.

CC This is a transposon sequence. The transposon comprises the genes
CC necessary for expression of resistance to glycopeptides in Enterococcus
CC faecium. It also contains genes associated with resistance, e.g. involved
CC in regulation of expression of the resistance genes or in the amount of
CC polypeptides produced. See also AAQ25179-025183. (Updated on 25-MAR-2003
CC to correct FN field.) (Updated on 25-MAR-2003 to correct FI field.)
CC (Updated on 24-OCT-2003 to standardise OS field)
XX SQ Sequence 10851 BP; 3399 A; 1960 C; 2234 G; 3258 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 27; DB 2; Length 10851;
XX Best Local Similarity 100.0%; Pred. No. 0.042; Mismatches 0;
XX Matches 27; Conservative 0; Indels 0; Gaps 0;
XX
XX 1 CCTATCCTGTTTGTAAAGCCGCGC 27
Db 7472 CCTATCCTGTTTGTAAAGCCGCGC 7498
XX
XX RESULT 21
XX AAF76019
XX ID AAF76019 standard; DNA; 10851 BP.
XX
XX AAF76019;
XX
XX 22-MAY-2001 (first entry)
XX
XX E. faecium VanA vancomycin resistance gene cluster, SEQ ID NO:1.
XX
XX Vancomycin resistance reduction; antisense expression inhibition;
XX competitive inducer sequestration; vanh promoter; vanR gene product;
XX Enterococcus; Staphylococcus; Streptococcus; Gram-positive bacterium;
XX antibiotic susceptibility; ex vivo eradication; in vivo eradication;
XX glycopeptide resistance; VanA gene cluster; de.
XX
XX Enterococcus faecium.
XX
XX WO200112803-A2.
XX
XX 22-FEB-2001.
XX
XX 11-AUG-2000; 2000MO-US022086.
XX
XX 17-AUG-1999; 99US-0149313P.
XX
XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
XX Inouye RT, Torres-Viera C, Moellering R, Gold H, Eliopoulos GM;
XX WPI; 2001-211216/21.
XX
XX Reducing vancomycin-resistance in vancomycin-resistant organism by
PT introducing a antisense vancomycin-resistance molecule to inhibit
PT vancomycin-resistance gene expression, or by enhancing vanh promoter
PT expression.
XX
XX Claim 24; Page 41-44; 59pp; English.
XX
XX The invention relates to methods of reducing vancomycin resistance in a
CC vancomycin-resistant organism. One method involves introducing a
CC vancomycin resistance gene antisense nucleic acid into the organism;
CC antisense oligonucleotides complementary to AAF76023-AAF76031 are
CC particularly preferred for this purpose. The second method involves
CC providing additional vanh promoter sequences which are not operatively
CC coupled to a vancomycin resistance gene, so that the phosphorylated vanR
CC gene product (which induces vanh promoter activity) is competitively
CC sequestered. Both methods are able to restore antibiotic susceptibility
CC in glycopeptide resistant enterococci. The methods of the invention are
CC useful for reducing vancomycin resistance in a vancomycin resistant
CC organism, particularly Enterococcus faecium and Enterococcus faecalis,
CC but also in other Gram-positive bacteria such as Staphylococcus sp. and
CC Streptococcus sp., to which Enterococcus faecium and Enterococcus
CC faecalis have the potential to transfer resistance determinants. The

antisease molecules are useful in the treatment of infection and colonization by vancomycin resistant enterococci and other clinically significant pathogens, and may be used for the ex vivo eradication of vancomycin-resistant enterococci from frequently colonised settings, such as intensive care units, haemodialysis units, and chronic care facilities; for the in vivo clearance of vancomycin-resistant enterococci from colonised gastrointestinal or genitourinary tracts of animals, including humans; and in primary or adjuvant therapy for vancomycin-resistant enterococcal infections. The gene based strategy targets key vancomycin resistance determinants and results in restoration of vancomycin susceptibility in previously glycopeptide-resistant enterococci. The present sequence represents the Enterococcus faecium Vana gene cluster

Sequence 10851 BP; 3392 A; 1962 C; 2237 G; 3260 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 10851;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCTATCCTGTTTGTGTAAGCCGCGC 27
7472 CCTATCCTGTTTGTGTAAGCCGCGC 7498

RESULT 22
ACA22997
ID ACA22997 standard; DNA; 1071 BP.
XX ACA22997;
XX
XX 19-JUN-2003 (first entry)
XX
XX Prokaryotic essential gene #4654.
XX
XX Antisense; ds; prokaryotic essential gene; cell proliferation;
XX drug design; gene.
XX
XX Borrelia burgdorferi.
XX
XX WO200277183-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
XX 06-SEP-2001; 2001US-00948893.
XX 25-OCT-2001; 2001US-0342923P.
XX 08-FEB-2002; 2002US-00072851.
XX 06-MAR-2002; 2002US-0362699P.
XX
XX (ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX MPI: 2003-029926/02.
XX P-PSDB; ABU19127.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
XX PT for homologous nucleic acids required for cellular proliferation to
XX PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 14; SEQ ID NO 10867; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding

the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 1071 BP; 335 A; 127 C; 198 G; 411 T; 0 U; 0 Other;

Query Match 77.0%; Score 20.8; DB 8; Length 1071;
Best Local Similarity 91.7%; Pred. No. 21;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 CTATCCTGTTTGTGTAAGCCGCGC 25
498 CTATCCTGTTTGTGTAAGCCGCGC 521

RESULT 23
AAK20248_07
Continuation (8 of 10) of AAK20248 from base 700001 (Borrelia burgdorferi polynucleotide
WP Sequence Split into 10 fragments LOCUS AAK20248 Accession AAK20248
WP Fragment Name Begin End
WP AAK20248_00 1 110000
WP AAK20248_01 100001 210000
WP AAK20248_02 200001 310000
WP AAK20248_03 300001 410000
WP AAK20248_04 400001 510000
WP AAK20248_05 500001 610000
WP AAK20248_06 600001 710000
WP AAK20248_07 700001 810000
WP AAK20248_08 800001 910000
WP AAK20248_09 900001 910715

Query Match 77.0%; Score 20.8; DB 2; Length 110000;
Best Local Similarity 91.7%; Pred. No. 41;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 CTATCCTGTTTGTGTAAGCCGCGC 25
10177 CTATCCTGTTTGTGTAAGCCGCGC 10200

RESULT 24
ADO47266/C
ID ADO47266 standard; DNA; 555 BP.
XX ADO47266;
XX
XX 15-JUN-2004 (first entry)
XX
XX Enterococcus vancomycin resistance gene, vanB ENEVANB2A.
XX
XX Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
XX gene; ds; hospital acquired infection; VRB;
XX fluorescence resonance energy transfer; FRET.
XX

```

XX OS Enterococcus sp.
XX PR US2004058336-A1.
XX PN
XX PD 25-MAR-2004.
XX PF 25-SEP-2002; 2002US-00254260.
XX PR 25-SEP-2002; 2002US-00254260.
XX PA (COCK/) COCKERILL F R.
XX PA (SLOA/) SLOAN L M.
XX PI Cockerill FR, Sloan LM;
XX DR WPI; 2004-268785/25.
XX PT Detecting presence or absence of vancomycin-resistant enterococci in
XX PT biological sample from individual comprises using real time polymerase
XX PT chain reaction.
XX PS Disclosure; SEQ ID NO 20; 23pp; English.
XX CC The invention relates to detecting the presence or absence of vancomycin-
XX CC resistant enterococci (VRE) in a sample, comprising performing a cycling
XX CC step by amplifying a sample with pair of vanA or vanB primers and
XX CC hybridising the sample with a pair of vanA or vanB probes, labelled with
XX CC donor and acceptor fluorescent group, respectively, detecting
XX CC fluorescence resonance energy transfer (FRET), where the presence of FRET
XX CC indicates presence of VRE. Also included is an article of manufacture,
XX CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
XX CC and a donor fluorescent group and a corresponding fluorescent group. The
XX CC method is useful for detecting the presence or absence of vancomycin-
XX CC resistant enterococci in a biological sample, e.g. stool samples, anal or
XX CC perirectal swabs, blood and body fluids from an individual. The method
XX CC replaces standard culture methods and reduces the cost. The method
XX CC provides rapid vancomycin resistant enterococcus real time PCR assay
XX CC which is useful for beginning the antimicrobial therapy immediately to
XX CC treat hospital acquired infection. The present sequence is an
XX CC enterococcal vanB, vancomycin resistance gene.
XX SQ Sequence 555 BP; 132 A; 161 C; 115 G; 145 T; 0 U; 2 Other;
XX
XX Query Match 76.3%; Score 20.6; DB 12; Length 555;
XX Best Local Similarity 85.2%; Pred. No. 23;
XX Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
XX Db 391 CCFACCTGTCTTGTGAAGCCGCGAC 365
XX
XX RESULT 25
XX ADO47264/C
XX ID ADO47264 standard; DNA; 556 BP.
XX AC ADO47264;
XX XX
XX DT 15-JUL-2004 (first entry)
XX DE Enterococcus vancomycin resistance gene, vanB ENEVANB.
XX OS Enterococcus vancomycin resistance gene; vanB ENEVANB.
XX KM Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
XX KM gene; ds; hospital acquired infection; VRE.
XX KM fluorescence resonance energy transfer; FRET.
XX OS Enterococcus sp.
XX XX
XX PN US2004058336-A1.
XX XX
XX PD 25-MAR-2004.
XX XX

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```

XX PF 25-SEP-2002; 2002US-00254260.
XX XX
XX PR 25-SEP-2002; 2002US-00254260.
XX XX
XX PA (COCK/) COCKERILL F R.
XX PA (SLOA/) SLOAN L M.
XX PI Cockerill FR, Sloan LM;
XX DR WPI; 2004-268785/25.
XX XX
XX PT Detecting presence or absence of vancomycin-resistant enterococci in
XX PT biological sample from individual comprises using real time polymerase
XX PT chain reaction.
XX PS Disclosure; SEQ ID NO 18; 23pp; English.
XX CC The invention relates to detecting the presence or absence of vancomycin-
XX CC resistant enterococci (VRE) in a sample, comprising performing a cycling
XX CC step by amplifying a sample with pair of vanA or vanB primers and
XX CC hybridising the sample with a pair of vanA or vanB probes, labelled with
XX CC donor and acceptor fluorescent group, respectively, detecting
XX CC fluorescence resonance energy transfer (FRET), where the presence of FRET
XX CC indicates presence of VRE. Also included is an article of manufacture,
XX CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
XX CC and a donor fluorescent group and a corresponding fluorescent group. The
XX CC method is useful for detecting the presence or absence of vancomycin-
XX CC resistant enterococci in a biological sample, e.g. stool samples, anal or
XX CC perirectal swabs, blood and body fluids from an individual. The method
XX CC replaces standard culture methods and reduces the cost. The method
XX CC provides rapid vancomycin resistant enterococcus real time PCR assay
XX CC which is useful for beginning the antimicrobial therapy immediately to
XX CC treat hospital acquired infection. The present sequence is an
XX CC enterococcal vanB, vancomycin resistance gene.
XX SQ Sequence 556 BP; 130 A; 154 C; 117 G; 155 T; 0 U; 0 Other;
XX
XX Query Match 76.3%; Score 20.6; DB 12; Length 556;
XX Best Local Similarity 85.2%; Pred. No. 23;
XX Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
XX Db 392 CCFACCTGTCTTGTGAAGCCGCGAC 366
XX
XX RESULT 26
XX ADO47262/C
XX ID ADO47262 standard; DNA; 556 BP.
XX AC ADO47262;
XX XX
XX DT 15-JUL-2004 (first entry)
XX DE E. faecalis vancomycin resistance gene, vanB EFT94526.
XX OS Enterococcus faecalis.
XX KM Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
XX KM gene; ds; hospital acquired infection; VRE.
XX KM fluorescence resonance energy transfer; FRET.
XX OS Enterococcus faecalis.
XX XX
XX PN US2004058336-A1.
XX XX
XX PD 25-MAR-2004.
XX XX
XX PF 25-SEP-2002; 2002US-00254260.
XX PR 25-SEP-2002; 2002US-00254260.
XX XX
XX PA (COCK/) COCKERILL F R.
XX PA (SLOA/) SLOAN L M.
XX XX

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PI Cockerill FR, Sloan LM;
 XX WPI; 2004-268785/25.
 DR
 PT Detecting presence or absence of vancomycin-resistant enterococci in
 PT biological sample from individual comprises using real time polymerase
 PT chain reaction.
 XX
 PS Disclosure; SEQ ID NO 15; 23bp; English.
 CC The invention relates to detecting the presence or absence of vancomycin-
 CC resistant enterococci (VRE) in a sample, comprising performing a cycling
 CC step by amplifying a sample with pair of vanA or vanB primers and
 CC hybridizing the sample with a pair of vanA or vanB probes, labelled with
 CC donor and acceptor fluorescent group, respectively, detecting
 CC fluorescence resonance energy transfer (FRET), where the presence of FRET
 CC indicates presence of VRE. Also included is an article of manufacture,
 CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
 CC and a donor fluorescent group and a corresponding fluorescent group. The
 CC method is useful for detecting the presence or absence of vancomycin-
 CC resistant enterococci in a biological sample, e.g. stool samples, anal or
 CC perirectal swabs, blood and body fluids from an individual. The method
 CC replaces standard culture methods and reduces the cost. The method
 CC provides rapid vancomycin resistant enterococcus real time PCR assay
 CC which is useful for beginning the antimicrobial therapy immediately to
 CC treat hospital acquired infection. The present sequence is an
 CC enterococcal vanB, vancomycin resistance gene.
 XX
 SQ Sequence 556 BP; 133 A; 162 C; 116 G; 145 T; 0 U; 0 Other;
 Query Match 76.3%; Score 20.6; DB 12; Length 556;
 Best Local Similarity 85.2%; Pred. No. 23;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
 DB 392 CCTACCTGTCTTTGTGAAGCCGCGAC 366
 RESULT 27
 ADO47263/c
 ID ADO47263 standard; DNA; 556 BP.
 XX
 AC ADO47263;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE E. faecalis vancomycin resistance gene, vanB EFU94527.
 XX
 KM Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
 KM gene; de; hospital acquired infection; VRE;
 KM fluorescence resonance energy transfer; FRET.
 XX
 OS Enterococcus faecalis.
 XX
 PN US2004058336-A1.
 PD 25-MAR-2004.
 XX
 PF 25-SEP-2002; 2002US-00254260.
 XX
 PR 25-SEP-2002; 2002US-00254260.
 XX
 PA (COCK/) COCKERILL F R.
 PA (SLOAN/) SLOAN L M.
 PI Cockerill FR, Sloan LM;
 DR WPI; 2004-268785/25.
 XX
 PT Detecting presence or absence of vancomycin-resistant enterococci in
 PT biological sample from individual comprises using real time polymerase
 PT chain reaction.

XX
 XX Disclosure; SEQ ID NO 17; 23bp; English.
 XX
 CC The invention relates to detecting the presence or absence of vancomycin-
 CC resistant enterococci (VRE) in a sample, comprising performing a cycling
 CC step by amplifying a sample with pair of vanA or vanB primers and
 CC hybridizing the sample with a pair of vanA or vanB probes, labelled with
 CC donor and acceptor fluorescent group, respectively, detecting
 CC fluorescence resonance energy transfer (FRET), where the presence of FRET
 CC indicates presence of VRE. Also included is an article of manufacture,
 CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
 CC and a donor fluorescent group and a corresponding fluorescent group. The
 CC method is useful for detecting the presence or absence of vancomycin-
 CC resistant enterococci in a biological sample, e.g. stool samples, anal or
 CC perirectal swabs, blood and body fluids from an individual. The method
 CC replaces standard culture methods and reduces the cost. The method
 CC provides rapid vancomycin resistant enterococcus real time PCR assay
 CC which is useful for beginning the antimicrobial therapy immediately to
 CC treat hospital acquired infection. The present sequence is an
 CC enterococcal vanB, vancomycin resistance gene.
 XX
 SQ Sequence 556 BP; 130 A; 154 C; 117 G; 155 T; 0 U; 0 Other;
 Query Match 76.3%; Score 20.6; DB 12; Length 556;
 Best Local Similarity 85.2%; Pred. No. 23;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
 DB 392 CCTACCTGTCTTTGTGAAGCCGCGAC 366
 RESULT 28
 ADO47261/c
 ID ADO47261 standard; DNA; 556 BP.
 XX
 AC ADO47261;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE E. faecalis vancomycin resistance gene, vanB EFU94529.
 XX
 KM Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
 KM gene; de; hospital acquired infection; VRE;
 KM fluorescence resonance energy transfer; FRET.
 XX
 OS Enterococcus faecalis.
 XX
 PN US2004058336-A1.
 PD 25-MAR-2004.
 XX
 PF 25-SEP-2002; 2002US-00254260.
 XX
 PR 25-SEP-2002; 2002US-00254260.
 XX
 PA (COCK/) COCKERILL F R.
 PA (SLOAN/) SLOAN L M.
 PI Cockerill FR, Sloan LM;
 DR WPI; 2004-268785/25.
 XX
 PT Detecting presence or absence of vancomycin-resistant enterococci in
 PT biological sample from individual comprises using real time polymerase
 PT chain reaction.
 XX
 PS Disclosure; SEQ ID NO 14; 23bp; English.
 XX
 CC The invention relates to detecting the presence or absence of vancomycin-
 CC resistant enterococci (VRE) in a sample, comprising performing a cycling
 CC step by amplifying a sample with pair of vanA or vanB primers and
 CC hybridizing the sample with a pair of vanA or vanB probes, labelled with

CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRB. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX
SQ Sequence 556 BP; 134 A; 161 C; 116 G; 145 T; 0 U; 0 Other;
Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
Db 392 CCTACCTGTTTGTGTAAGCCGCGCAC 366
RESULT 29
AD047265/c
ID AD047265 standard; DNA; 556 BP.
XX
AC AD047265;
XX
DT 15-JUL-2004 (first entry)
XX
DE E. faecalis vancomycin resistance gene, vanB EFU72704.
XX
XX Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KM gene; ds; hospital acquired infection; VRB;
KM fluorescence resonance energy transfer; FRET.
XX
OS Enterococcus faecalis.
XX
PN US2004058336-A1.
XX
PD 25-MAR-2004.
XX
PF 25-SEP-2002; 2002US-00254260.
XX
PR 25-SEP-2002; 2002US-00254260.
XX
PA (COCK/) COCKERILL F R.
PA (SLOAN/) SLOAN L M.
XX
PI Cockerill FR, Sloan LM;
PT
DR WPI; 2004-268785/25.
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 19; 23pp; English.
XX
XX The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridizing the sample with a pair of vanA or vanB probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRB. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX

CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX
SQ Sequence 556 BP; 134 A; 158 C; 117 G; 147 T; 0 U; 0 Other;
Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
Db 392 CCTACCTGTTTGTGTAAGCCGCGCAC 366
RESULT 30
AD047260/c
ID AD047260 standard; DNA; 556 BP.
XX
AC AD047260;
XX
DT 15-JUL-2004 (first entry)
XX
DE E. faecalis vancomycin resistance gene, vanB EFU94528.
XX
XX Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KM gene; ds; hospital acquired infection; VRB;
KM fluorescence resonance energy transfer; FRET.
XX
OS Enterococcus faecalis.
XX
PN US2004058336-A1.
XX
PD 25-MAR-2004.
XX
PF 25-SEP-2002; 2002US-00254260.
XX
PR 25-SEP-2002; 2002US-00254260.
XX
PA (COCK/) COCKERILL F R.
PA (SLOAN/) SLOAN L M.
XX
PI Cockerill FR, Sloan LM;
PT
DR WPI; 2004-268785/25.
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 13; 23pp; English.
XX
XX The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanA or vanB primers and
CC hybridizing the sample with a pair of vanA or vanB probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRB. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.
XX

SO Sequence 556 BP; 134 A; 161 C; 116 G; 145 T; 0 U; 0 Other;

Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
DB 392 CCTACCTGCTTTGTGAAGCGGCGAC 366

RESULT 31

ADO47259/c
ID ADO47259 standard; DNA; 556 BP.

AC ADO47259;

DT 15-JUN-2004 (first entry)

DE E. faecalis vancomycin resistance gene, vanB BRU94530.

XX Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;

KW gene; ds; hospital acquired infection; VRB;

KW fluorescence resonance energy transfer; FRRT.

XX Enterococcus faecalis.

XX US2004058336-A1.

XX 25-MAR-2004.

XX 25-SEP-2002; 2002US-00254260.

XX 25-SEP-2002; 2002US-00254260.

XX (COCK/) COCKERILL F. R.

XX (SLOA/) SLOAN L. M.

XX Cockerill FR, Sloan LM;

XX WPI; 2004-268785/25.

XX WPI; 2004-268785/25.

XX WPI; 2004-268785/25.

XX WPI; 2004-268785/25.

XX WPI; 2004-268785/25.

XX WPI; 2004-268785/25.

XX WPI; 2004-268785/25.

XX WPI; 2004-268785/25.

XX WPI; 2004-268785/25.

XX WPI; 2004-268785/25.

XX WPI; 2004-268785/25.

XX WPI; 2004-268785/25.

XX WPI; 2004-268785/25.

XX WPI; 2004-268785/25.

XX WPI; 2004-268785/25.

XX WPI; 2004-268785/25.

XX WPI; 2004-268785/25.

DB 392 CCTACCTGCTTTGTGAAGCGGCGAC 366

RESULT 32
AAQ69230
ID AAQ69230 standard; DNA; 589 BP.

XX AAQ69230;

DT 25-MAR-2003 (revised)

DT 23-FEB-1995 (first entry)

XX Enterococcus faecalis vanB gene (internal, amplified fragment).

XX Gram positive bacteria; inducible glycopeptide resistance; vancomycin;

XX teicoplanin; antibiotic; vanB gene; ds.

XX Enterococcus faecalis.

XX Key Location/Qualifiers

XX Key misc_feature 2.589

XX FR2699539-A1.

XX 24-JUN-1994.

XX 18-DEC-1992; 92PR-00015671.

XX 18-DEC-1992; 92PR-00015671.

XX (INSP) INST PASTEUR.

XX Arthur M, Dutka-Malen S, Evers S, Courvalin P;

XX WPI; 1994-227159/28.

XX P-PSDB; AAR57150.

XX New protein VanB involved in bacterial resistance to glyco-peptide(s) -

XX esp vancomycin, and related nucleic acid, vectors, transformed cells and

XX antibodies, for in vitro detection of resistant strains.

XX Claim 8; Page 28; 39pp; French.

XX The protein encoded by the vanB gene is implicated in resistance of Gram-

XX positive bacteria to glycopeptides, particularly to vancomycin. This

XX resistance is inducible by Vancomycin but not by teicoplanin. Sequence

XX AAQ69230 is a claimed internal fragment of the vanB gene. (Updated on 25-

XX MAR-2003 to correct PN field.)

XX Sequence 589 BP; 163 A; 124 C; 166 G; 136 T; 0 U; 0 Other;

XX Query Match 76.3%; Score 20.6; DB 2; Length 589;

XX Best Local Similarity 85.2%; Pred. No. 23;

XX Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTGTAAGCGGCGC 27

DB 165 CCTACCTGCTTTGTGAAGCGGCGAC 191

XX RESULT 33

XX ADY59941

XX ADY59941 standard; DNA; 630 BP.

XX ADY59941;

XX 02-JUN-2005 (first entry)

XX Enterococcus faecalis vanB DNA sequence SEQ ID NO:15.

Query Match	Best Local Similarity	Score	DB	Length
Matches	23; Conservative	85.2%;	0; Mismatches	4; Indels
			0; Gaps	0;
1 CCTATCCGTGTTTGTTAAGCCGCGCC	27			
Db	185 CCTACCTGTCTTGTGTAAGCGGAC	211		
Sequence	630 BP; 163 A; 135 C; 187 G; 145 T; 0 U; 0 Other;			
Query Match	76.3%;	Score 20.6;	DB 14;	Length 630;
Best Local Similarity	85.2%;	Pred. No. 24;		
Matches	23; Conservative	0; Mismatches	4; Indels	0; Gaps
1 CCTATCCGTGTTTGTTAAGCCGCGCC	27			
Db	185 CCTACCTGTCTTGTGTAAGCGGAC	211		
Sequence	630 BP; 163 A; 135 C; 187 G; 145 T; 0 U; 0 Other;			
Query Match	76.3%;	Score 20.6;	DB 14;	Length 630;
Best Local Similarity	85.2%;	Pred. No. 24;		
Matches	23; Conservative	0; Mismatches	4; Indels	0; Gaps
1 CCTATCCGTGTTTGTTAAGCCGCGCC	27			
Db	185 CCTACCTGTCTTGTGTAAGCGGAC	211		
Sequence	630 BP; 163 A; 135 C; 187 G; 145 T; 0 U; 0 Other;			
Query Match	76.3%;	Score 20.6;	DB 14;	Length 630;
Best Local Similarity	85.2%;	Pred. No. 24;		
Matches	23; Conservative	0; Mismatches	4; Indels	0; Gaps
1 CCTATCCGTGTTTGTTAAGCCGCGCC	27			
Db	185 CCTACCTGTCTTGTGTAAGCGGAC	211		
Sequence	630 BP; 163 A; 135 C; 187 G; 145 T; 0 U; 0 Other;			
Query Match	76.3%;	Score 20.6;	DB 14;	Length 630;
Best Local Similarity	85.2%;	Pred. No. 24;		
Matches	23; Conservative	0; Mismatches	4; Indels	0; Gaps
1 CCTATCCGTGTTTGTTAAGCCGCGCC	27			
Db	185 CCTACCTGTCTTGTGTAAGCGGAC	211		
Sequence	630 BP; 163 A; 135 C; 187 G; 145 T; 0 U; 0 Other;			
Query Match	76.3%;	Score 20.6;	DB 14;	Length 630;
Best Local Similarity	85.2%;	Pred. No. 24;		
Matches	23; Conservative	0; Mismatches	4; Indels	0; Gaps
1 CCTATCCGTGTTTGTTAAGCCGCGCC	27			
Db	185 CCTACCTGTCTTGTGTAAGCGGAC	211		
Sequence	630 BP; 163 A; 135 C; 187 G; 145 T; 0 U; 0 Other;			
Query Match	76.3%;	Score 20.6;	DB 14;	Length 630;
Best Local Similarity	85.2%;	Pred. No. 24;		
Matches	23; Conservative	0; Mismatches	4; Indels	0; Gaps
1 CCTATCCGTGTTTGTTAAGCCGCGCC	27			
Db	185 CCTACCTGTCTTGTGTAAGCGGAC	211		
Sequence	630 BP; 163 A; 135 C; 187 G; 145 T; 0 U; 0 Other;			
Query Match	76.3%;	Score 20.6;	DB 14;	Length 630;
Best Local Similarity	85.2%;	Pred. No. 24;		
Matches	23; Conservative	0; Mismatches	4; Indels	0; Gaps
1 CCTATCCGTGTTTGTTAAGCCGCGCC	27			
Db	185 CCTACCTGTCTTGTGTAAGCGGAC	211		
Sequence	630 BP; 163 A; 135 C; 187 G; 145 T; 0 U; 0 Other;			
Query Match	76.3%;	Score 20.6;	DB 14;	Length 630;
Best Local Similarity	85.2%;	Pred. No. 24;		
Matches	23; Conservative	0; Mismatches	4; Indels	0; Gaps
1 CCTATCCGTGTTTGTTAAGCCGCGCC	27			
Db	185 CCTACCTGTCTTGTGTAAGCGGAC	211		
Sequence	630 BP; 163 A; 135 C; 187 G; 145 T; 0 U; 0 Other;			
Query Match	76.3%;	Score 20.6;	DB 14;	Length 630;
Best Local Similarity	85.2%;	Pred. No. 24;		
Matches	23; Conservative	0; Mismatches	4; Indels	0; Gaps
1 CCTATCCGTGTTTGTTAAGCCGCGCC	27			
Db	185 CCTACCTGTCTTGTGTAAGCGGAC	211		
Sequence	630 BP; 163 A; 135 C; 187 G; 145 T; 0 U; 0 Other;			
Query Match	76.3%;	Score 20.6;	DB 14;	Length 630;
Best Local Similarity	85.2%;	Pred. No. 24;		
Matches	23; Conservative	0; Mismatches	4; Indels	0; Gaps
1 CCTATCCGTGTTTGTTAAGCCGCGCC	27			

Query Match	Best Local Similarity	Score	DB	Length	763;
Matches	23; Conservative	0;	Mismatches	4;	Indels
		0;	Gaps	0;	
QY	1	CCATCCTCTTTTGTGAAGCCGCGC	27		
DB	392	CCATCCTCTTTTGTGAAGCCGCGC	418		
RESULT 35					
ID	AAH01126	standard; DNA; 801 BP.			
XX	AAH01126;				
XX	24-JUL-2001	(first entry)			
XX	DT				
XX	Enterococcus faecium	nucleotide sequence SEQ ID NO:1117.			
XX	Species specific;	genus specific; family specific; probe; detection;			
XX	identification;	algal; archaeal; bacterial; fungal; parasitic;			
XX	microorganism;	diagnosis; translation elongation factor Tu; toxin;			
XX	translation elongation factor G;	RecA recombinase; resistance;			
XX	catalytic subunit of proton-translocating ATPase;	antimicrobial; vaccine;			
XX	primer; ds.				
XX	Enterococcus faecium.				
XX	WO200123604-A2.				

XX 05-APR-2001.
 PD 28-SEP-2000; 2000MO-CA001150.
 XX 28-SEP-1999; 99CA-02283458.
 PR 19-MAR-2000; 2000CA-02307010.
 XX (INPR-) INFECTIO DIAGNOSTIC (IDI) INC.
 PA Bergeron MG, Bolesnot M, Huletsky A, Menard C, Ouellette M;
 PI Picard RJ, Roy PH;
 XX WPI; 2001-245006/25.
 DR Nucleic acid sequences are used to generate universal probes and primers
 XX which can be used to identify and detect the presence of algal, archaeal,
 PT bacterial, fungal and parasitological species in a test sample.
 PT Disclosure; Page 1027; 1580pp; English.

XX The present invention describes a method for generating a repository of
 CC nucleic acids of tuf, fts, atp and/or recA genes from which probes
 CC and/or primers are derived. The method comprises amplifying the nucleic
 CC acids of determined algal, archaeal, bacterial, fungal and parasitological
 CC species with a combination of defined primer pairs. The method can be
 CC used for producing probes and/or primers for detecting one or more
 CC related microorganisms e.g. algae, archaea, bacteria, fungi and
 CC parasites, for universal detection and for specific and ubiquitous
 CC detection and identification of an algal, archaeal, bacterial, fungal and
 CC parasitological species, genus, family and group. A nucleic acid (I) obtained
 CC using the method of the invention can be used for the universal detection
 CC of any bacterium, fungus or parasite in a sample and for the detection of
 CC at least one antimicrobial agent resistance gene or at least one toxin
 CC gene. hexa nucleic acids are used for the specific and ubiquitous
 CC detection and for identification of Streptococcus pneumoniae. (I) can be
 CC used to design a therapeutic agent which is effective against
 CC microorganisms. Microbial species or genus or family or phylum or group
 CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
 CC Corynebacterium sp., Enterobacteriaceae group, Bacillus coli,
 CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
 CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
 CC results than substrate specificity tests as results can be determined in
 CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
 CC represent nucleotide sequences and primers/probes which are given in the
 CC exemplification of the present invention.

XX Sequence 801 BP; 215 A; 169 C; 235 G; 182 T; 0 U; 0 Other;

XX Query Match 76.3%; Score 20.6; DB 4; Length 801;
 XX Best Local Similarity 85.2%; Pred. No. 25;
 XX Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCTATCCCTTTTGTGTAAGCCGCGC 27
 DB 389 CCTACCTGTCTTGTGAAGCCGCGAC 415

XX RESULT 36
 XX ADY59937/c
 XX ID ADY59937 standard; DNA; 801 BP.

XX AC ADY59937;

XX DT 02-JUN-2005 (first entry)

XX DE Enterococcus faecium vanB DNA sequence SEQ ID NO:11.

XX KM DNA detection; antibiotic-resistance; vancomycin; vanB; de.

XX OS Enterococcus faecium.

XX PN US2005058985-A1.

XX 17-MAR-2005.
 PD 12-SEP-2003; 2003US-00661094.
 XX 12-SEP-2003; 2003US-00661094.
 PR 12-SEP-2003; 2003US-00661094.
 XX (DODG/) DODGSON K J.
 PA Dodgson KJ;
 PI WPI; 2005-222218/23.
 DR Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
 XX e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
 PT and/or vanB-specific oligonucleotide probes or primers.
 PT Example 1; SEQ ID NO 11; 33pp; English.

XX The invention relates to a method for detecting vancomycin resistance
 CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
 CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
 CC probe or primer, and detecting or determining the presence or amount of
 CC hybrid formation or amplified nucleic acid. Also described: (1) an
 CC oligonucleotide composition comprising a first oligonucleotide comprising
 CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
 CC 898-917 of the vanA gene, or its complement or portion, or an
 CC oligonucleotide comprising sequences substantially corresponding to
 CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
 CC complement or portion, where the oligonucleotide hybridizes under
 CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
 CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
 CC vanB gene in a test sample, comprising the oligonucleotide mentioned
 CC above. The method and kit are useful for detecting and/or amplifying
 CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
 CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
 CC They may also be used in other industrial purposes, such as for quality
 CC control of food, water, pharmaceutical products or other products
 CC requiring microbiological control. The present sequence represents an
 CC Enterococcus faecium vanB nucleotide sequence from the present invention.

XX Sequence 801 BP; 181 A; 226 C; 169 G; 225 T; 0 U; 0 Other;

XX Query Match 76.3%; Score 20.6; DB 14; Length 801;
 XX Best Local Similarity 85.2%; Pred. No. 25;
 XX Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCTATCCCTTTTGTGTAAGCCGCGC 27
 DB 413 CCTACCTGTCTTGTGAAGCCGCGAC 387

XX RESULT 37
 XX ADY59940/c
 XX ID ADY59940 standard; DNA; 801 BP.

XX AC ADY59940;

XX DT 02-JUN-2005 (first entry)

XX DE Enterococcus faecium vanB DNA sequence SEQ ID NO:14.

XX KM DNA detection; antibiotic-resistance; vancomycin; vanB; de.

XX OS Enterococcus faecium.

XX PN US2005058985-A1.

XX DT 17-MAR-2005.

XX PF 12-SEP-2003; 2003US-00661094.

XX PR 12-SEP-2003; 2003US-00661094.

PA	(DODG/) DODGSON K J.
PX	Dodgson KJ;
PI	
XX	WP1; 2005-222218/23.
DR	
PT	Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for e.g., identifying vancomycin-resistant enterococcus, comprising using vanA-and/or vanB-specific oligonucleotide probes or primers.
PS	Example 1, SEQ ID NO 14; 33pp; English.
XS	The invention relates to a method for detecting vancomycin resistance gene vanA and/or vanB nucleic acid molecules in a sample comprising contacting the sample with a vanA- and/or vanB-specific oligonucleotide probe or primer, and detecting or determining the presence or amount of hybrid formation or amplified nucleic acid. Also described: (1) an oligonucleotide composition comprising a first oligonucleotide comprising sequences substantially corresponding to nucleotides 870-896, 851-868 or 898-917 of the vanA gene, or its complement or portion, or an oligonucleotide comprising sequences substantially corresponding to CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its complement or portion, where the oligonucleotide hybridizes under stringent hybridization conditions to vanA or vanB DNA; and (2) a kit comprising one or more oligonucleotide(s) specific for a vanA gene and/or vanB gene in a test sample, comprising the oligonucleotide mentioned above. The method and kit are useful for detecting and/or amplifying genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC	They may also be used in other industrial purposes, such as for quality control of food, water, pharmaceutical products or other products requiring microbiological control. The present sequence represents an Enterococcus faecium vanB nucleotide sequence from the present invention.
SC	
SQ	Sequence 801 BP; 183 A; 234 C; 169 G; 215 T; 0 U; 0 Other; Query Match 76.3%; Score 20.6; DB 14; Length 801; Best Local Similarity 85.2%; Pred. No. 25; Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0. 1 CCTATCCTGTTTTGGTAAGCGGC 27 Db 413 CTACCTGTCTTGGAAGCGGC 387
OY	
RESULT 38	
ID	ADVS9943/C
AD	ADVS9943 standard; DNA; 801 BP.
AC	ADVS9943;
XX	
DT	02-JUN-2005 (first entry)
XX	
XE	Consensus vanB DNA sequence SEQ ID NO:14.
XX	
KW	DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
OS	Enterococcus faecium.
OS	Enterococcus faecalis.
OS	Synthetic.
PN	US2005058985-A1.
PD	
PD	17-MAR-2005.
PF	12-SEP-2003; 2003US-00661094.
PR	12-SEP-2003; 2003US-00661094.
PA	(DODG/) DODGSON K J.
PI	Dodgson KJ,

Query Match	Best Local Similarity	76.3%	Score 20.6	DB 14	Length 801
Matches 23	Conservative 0	Mismatches 4	Indels 0	Gaps 0	
Qy	1 CCTATCCTGTTTGTTAAGCCGCGC 27				
Db	413 CCTATCCTGTTTGTTAAGCCGCGC 387				
<p>RESULT 39</p> <p>ADY59939/c</p> <p>ID ADY59939 standard; DNA; 801 BP.</p> <p>XX ADY59939;</p> <p>XX</p> <p>DT 02-JUN-2005 (first entry)</p> <p>XX</p> <p>DE Enterococcus faecium vanB DNA sequence SEQ ID NO:13.</p> <p>XX</p> <p>KW DNA detection; antibiotic-resistance; vancomycin; vanB; ds.</p> <p>XX</p> <p>OS Enterococcus faecium.</p> <p>XX</p> <p>PN US2005058985-A1.</p> <p>XX</p> <p>PD 17-MAR-2005.</p> <p>XX</p> <p>PE 12-SEP-2003; 2003US-00661094.</p> <p>XX</p> <p>PR 12-SEP-2003; 2003US-00661094.</p> <p>XX</p> <p>PA (DODG/) DODGSON K J.</p> <p>XX</p> <p>PI Dodgson KJ;</p> <p>XX</p> <p>DR WP1; 2005-222218/23.</p> <p>XX</p> <p>PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for</p> <p>PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-</p> <p>PT and/or vanB-specific oligonucleotide probes or primers.</p> <p>XX</p> <p>Example 1; SEQ ID NO 17; 33pp; English.</p> <p>XX</p> <p>The invention relates to a method for detecting vancomycin resistance</p> <p>CC gene vanA and/or vanB nucleic acid molecules in a sample comprising</p> <p>CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide</p> <p>CC probe or primer, and detecting or determining the presence or amount of</p> <p>CC hybrid formation or amplified nucleic acid. Also described: (1) an</p> <p>CC oligonucleotide composition comprising a first oligonucleotide comprising</p> <p>CC sequences substantially corresponding to nucleotides 870-896, 851-868 or</p> <p>CC 898-917 of the vanA gene, or its complement or portion, or an</p> <p>CC oligonucleotide comprising sequences substantially corresponding to</p> <p>CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its</p> <p>CC complement or portion, where the oligonucleotide hybridizes under</p> <p>CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit</p> <p>CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or</p> <p>CC vanB gene in a test sample, comprising the oligonucleotide mentioned</p> <p>CC above. The method and kit are useful for detecting and/or amplifying</p> <p>CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying</p> <p>CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).</p> <p>CC They may also be used in other industrial purposes, such as for quality</p> <p>CC control of food, water, pharmaceutical products or other products</p> <p>CC requiring microbiological control. The present sequence represents a</p> <p>CC consensus vanB nucleotide sequence from the present invention.</p> <p>XX</p> <p>Sequence 801 BP; 181 A; 235 C; 169 G; 216 T; 0 U; 0 Other;</p>					

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2006, 06:01:49 ; Search time 1049.14 Seconds

(without alignments)
1462.883 Million cell updates/sec

Title: US-10-661-094-3

Perfect score: 27

Sequence: 1 cctatccgttttctgtaagccgagcgc 27

Scoring table: IDENTITY_NUC

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 120 summaries

Database :

GenBank1:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hcg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	27	6 CS061875	CS061875 Sequence
2	27	100.0	614	1 AY754011	AY754011 Enterococ
3	27	100.0	1029	6 AR035505	AR035505 Sequence
4	27	100.0	1029	6 BD181846	BD181846 Polypepti
5	27	100.0	1032	1 AY648035	AY648035 Penicbact
6	27	100.0	1032	1 AY648698	AY648698 Penicbact
7	27	100.0	1032	6 AX085668	AX085668 Sequence
8	27	100.0	1032	6 AX111560	AX111560 Sequence
9	27	100.0	1034	6 CQ797595	CQ797595 Sequence
10	27	100.0	1218	6 AX110322	AX110322 Sequence
11	27	100.0	1232	6 AX110321	AX110321 Sequence
12	27	100.0	1237	6 AX110319	AX110319 Sequence
13	27	100.0	1241	6 AX110316	AX110316 Sequence
14	27	100.0	1249	6 AX110317	AX110317 Sequence
15	27	100.0	1263	6 AX110320	AX110320 Sequence
16	27	100.0	1265	6 AX110323	AX110323 Sequence
17	27	100.0	1269	6 AX110324	AX110324 Sequence
18	27	100.0	1272	6 AX110318	AX110318 Sequence

19	27	100.0	1768	1 EFPVANAG	X56895 E.faecium P
20	27	100.0	1768	6 CQ797596	CQ797596 Sequence
21	27	100.0	1768	6 CQ797597	CQ797597 Sequence
22	27	100.0	1768	6 CS061873	CS061873 Sequence
23	27	100.0	1768	6 AX110406	AX110406 Sequence
24	27	100.0	2607	6 AR089411	AR089411 Sequence
25	27	100.0	2607	6 AR093611	AR093611 Sequence
26	27	100.0	2667	6 AR035514	AR035514 Sequence
27	27	100.0	2667	6 BD181855	BD181855 Polypepti
28	27	100.0	3446	6 AX110408	AX110408 Sequence
29	27	100.0	4654	1 AY926880	AY926880 Penicbact
30	27	100.0	7225	6 AR035512	AR035512 Sequence
31	27	100.0	7225	6 BD181853	BD181853 Polypepti
32	27	100.0	9519	1 DQ018711	DQ018711 Penicbact
33	27	100.0	9537	1 DQ018710	DQ018710 Penicbact
34	27	100.0	10851	1 TRNVAN	M97297 Enterococcu
35	27	100.0	10851	6 AR035513	AR035513 Sequence
36	27	100.0	10851	6 BD181854	BD181854 Polypepti
37	27	100.0	10851	6 AX085648	AX085648 Sequence
38	27	100.0	17510	1 AP516335	AP516335 Enterococ
39	27	100.0	57889	1 AE017171	AE017171 Staphyloc
40	25.4	94.1	1054	1 BCY15704	Y15704 Bacillus ci
41	23.8	88.1	786	1 CP000013_2	X79049 O.turkaba P
42	23.8	88.1	9537	1 AF155139	AF155139 Penicbact
43	21.2	78.5	648	10 BV376857	BV376857 S231P613R
44	20.8	77.0	12663	1 AE001130	AE001130 Borrelia
45	20.8	77.0	110000	1 CP000013_1	Continuation (2 of
46	20.8	77.0	110000	1 CP000013_2	Continuation (3 of
47	20.6	76.3	264	1 AY969704	AY969704 Staphyloc
48	20.6	76.3	365	1 AY697424	AY697424 Enterococ
49	20.6	76.3	438	1 AY035703	AY035703 Streptococ
50	20.6	76.3	438	1 AY035704	AY035704 Streptococ
51	20.6	76.3	438	1 AY035705	AY035705 Streptococ
52	20.6	76.3	552	1 AY786179	AY786179 Enterococ
53	20.6	76.3	556	6 CQ797599	CQ797599 Sequence
54	20.6	76.3	556	6 CQ797600	CQ797600 Sequence
55	20.6	76.3	556	6 CQ797601	CQ797601 Sequence
56	20.6	76.3	556	6 CQ797602	CQ797602 Sequence
57	20.6	76.3	556	6 CQ797603	CQ797603 Sequence
58	20.6	76.3	556	6 CQ797604	CQ797604 Sequence
59	20.6	76.3	556	6 CQ797605	CQ797605 Sequence
60	20.6	76.3	556	6 CQ797606	CQ797606 Sequence
61	20.6	76.3	589	1 ENRVANB	L06138 Enterococcu
62	20.6	76.3	589	6 A39314	A39314 Sequence 4
63	20.6	76.3	589	6 AR102788	AR102788 Sequence
64	20.6	76.3	589	6 AR338261	AR338261 Sequence
65	20.6	76.3	630	1 ENRVANB2A	L15304 Enterococcu
66	20.6	76.3	630	6 CS061887	CS061887 Sequence
67	20.6	76.3	635	1 SHVANB2	Z70527 S.bovis bio
68	20.6	76.3	671	1 AY704417	AY704417 Enterococ
69	20.6	76.3	732	1 AY665551	AY665551 Enterococ
70	20.6	76.3	783	1 BFU72704	U72704 Enterococcu
71	20.6	76.3	783	6 CS061888	CS061888 Sequence
72	20.6	76.3	801	1 BFU94526	U94526 Enterococcu
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74	20.6	76.3	801	1 BFU94528	U94528 Enterococcu
75	20.6	76.3	801	1 BFU94529	U94529 Enterococcu
76	20.6	76.3	801	1 BFU94530	U94530 Enterococcu
77	20.6	76.3	801	6 CS061882	CS061882 Sequence
78	20.6	76.3	801	6 CS061883	CS061883 Sequence
79	20.6	76.3	801	6 CS061884	CS061884 Sequence
80	20.6	76.3	801	6 CS061885	CS061885 Sequence
81	20.6	76.3	801	6 CS061886	CS061886 Sequence
82	20.6	76.3	801	6 CS061889	CS061889 Sequence
83	20.6	76.3	801	6 AX110384	AX110384 Sequence
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85	20.6	76.3	882	6 CQ797598	CQ797598 Sequence
86	20.6	76.3	1029	1 AF310953	AF310953 Enterococ
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88	20.6	76.3	1029	1 AF310955	AF310955 Enterococ
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92 20.6 76.3 1029 1 AY655711 Enterococ
KEYWORDS AY655712 Clostridi
SOURCE AY655713 Clostridi
ORGANISM AY655714 Ruminococ
AY655715 Clostridi
AY655716 Clostridi
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ALIGNMENTS

RESULT 1
LOCUS CS061875 27 bp DNA linear PAT 13-APR-2005
DEFINITION Sequence 3 from Patent WO2005028679.
ACCESSION CS061875
VERSION CS061875.1 GI:62553769

KEYWORDS Enterococcus faecium
SOURCE Enterococcus faecium
ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.
REFERENCE 1
AUTHORS Dodgson, K.J.
TITLE Method and kit for identifying vancomycin-resistant enterococcus
JOURNAL Patent: WO 2005028679-A 3 31-MAR-2005;
University of Iowa Research Foundation (US); DODGSON, Kirsty Jane
(US)

FEATURES
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/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 CCTATCCTGTTTGTGTTAAGCCGCGC 27
1 CCTATCCTGTTTGTGTTAAGCCGCGC 27

RESULT 2
LOCUS AY754011 614 bp DNA linear BCT 19-JAN-2005
DEFINITION Enterococcus faecium vancomycin resistance protein A (vna) gene,
ACCESSION AY754011

VERSION AY754011.1 GI:57790303
KEYWORDS Enterococcus faecium
SOURCE Enterococcus faecium
ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE 1 (bases 1 to 614)
AUTHORS Knudsen, B.Y., Shafiani, S., Tewari, R. and Taneja, N.
TITLE Detection and molecular characterization of vancomycin resistance
genes from clinical strains of Enterococci

JOURNAL Unpublished
2 (bases 1 to 614)
AUTHORS Knudsen, B.Y., Shafiani, S., Tewari, R. and Taneja, N.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2004) Biotechnology, Panjab University,
Sector-14, Chandigarh, U.T. 160014, India

FEATURES
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Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
LOCUS AR035505 1029 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5871910.
ACCESSION AR035505
VERSION AR035505.1 GI:5952173

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1029)
AUTHORS Arthur, M., Dutka-Malen, S., Molinas, C. and Courvalin, P.
TITLE Probes for the detection of nucleotide sequences implicated in the
expression of resistance to glycopeptides, in particular in
gram-positive bacteria

JOURNAL Patent: US 5871910-A 3 16-FEB-1999;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 CCTATCCTGTTTGTGTTAAGCCGCGC 27

DB 494 CCTATCCTGTTTGTGTAAGCCGCGC 520

RESULT 4
LOCUS BD181846
DEFINITION Polypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nucleotide sequence coding for these polypeptides and use for diagnosis.

ACCESSION BD181846
VERSION BD181846.1 GI:30792764
KEYWORDS JP 2002320494-A/2.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 1029)
AUTHORS Arthur, M., Dukcamalen, S., Molina, C. and Courvalin, P.
TITLE Polypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nucleotide sequence coding for these polypeptides and use for diagnosis
JOURNAL Patent: JP 2002320494-A 2 05-NOV-2002;
INSTITUT PASTEUR
OS Bacteria
PN JP 2002320494-A/2
PD 05-NOV-2002
PF 21-FEB-2002 JP 2002045484
PR 31-OCT-1990 FR 90/13579
PI MICHEL, ARTHUR, SYLVIE, DUKTA-MALEN, CATHERINE MOLINAS, PATRICE PI
COURVALIN
PC C12N15/09, C07K14/315, C07K16/12, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12Q1/04, C12Q1/68, G01N33/53, G01N33/566, G01N33/569//C12P21/08,
PC C12Q1/04, C12R1/01, C12Q1/68, C12R1/01, C12N15/00, C12N5/00 CC
Polypeptides implicated in the expression of resistance to CC
glycopeptides,
CC in particular in gram-positive bacteria, nucleotide sequence
CC coding for
CC these polypeptides and use for diagnosis
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ORIGIN
Query Match 100.0%; Score 27; DB 6; Length 1029;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
DB 494 CCTATCCTGTTTGTGTAAGCCGCGC 520

RESULT 5
LOCUS AY648035
DEFINITION Paenibacillus thiaminolyticus D-alanyl-D-alanine ligase gene, complete cds.

ACCESSION AY648035
VERSION AY648035.1 GI:50082936
KEYWORDS Paenibacillus thiaminolyticus
SOURCE Paenibacillus thiaminolyticus
ORGANISM Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
REFERENCE 1 (bases 1 to 1032)
AUTHORS Guardabassi, L., Christensen, H., Hasman, H. and Dalsgaard, A.
TITLE Members of the Genus Paenibacillus and Rhodococcus Harbor Genes Homologous to Enterococcal Glycopeptide Resistance Genes vanA and vanB

JOURNAL Antimicrob. Agents Chemother. 48 (12), 4915-4918 (2004)
PUBMED 15561881
REFERENCE 2 (bases 1 to 1032)
AUTHORS Guardabassi, L., Hasman, H., Christensen, H. and Dalsgaard, A.
TITLE Direct Submission
JOURNAL Submitted (08-JUN-2004) Veterinary Pathobiology, The Royal Veterinary and Agricultural University, Stigboejlen 4, Frederiksberg C 1870, Denmark

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/db_xref="GI:50082937"
/translation="MNRKVAIIPGGSEBHDVSKSAREIANIDNEKTEPLTIGIT
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
DB 494 CCTATCCTGTTTGTGTAAGCCGCGC 520

RESULT 6
LOCUS AY648698
DEFINITION Paenibacillus apiarius D-alanyl-D-alanine ligase gene, complete cds.

ACCESSION AY648698
VERSION AY648698.1 GI:50082942
KEYWORDS Paenibacillus apiarius
SOURCE Paenibacillus apiarius
ORGANISM Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
REFERENCE 1 (bases 1 to 1032)
AUTHORS Guardabassi, L., Christensen, H., Hasman, H. and Dalsgaard, A.
TITLE Members of the Genus Paenibacillus and Rhodococcus Harbor Genes Homologous to Enterococcal Glycopeptide Resistance Genes vanA and vanB

JOURNAL Antimicrob. Agents Chemother. 48 (12), 4915-4918 (2004)
PUBMED 15561881
REFERENCE 2 (bases 1 to 1032)
AUTHORS Guardabassi, L., Hasman, H., Christensen, H. and Dalsgaard, A.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-2004) Veterinary Pathobiology, The Royal Veterinary and Agricultural University, Stigboejlen 4, Frederiksberg C 1870, Denmark

FEATURES
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/mol_type="genomic DNA"
/strain="PA-B28"
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/protein_id="AAU70093.1"

ORIGIN	Query Match	Best Local	Matches	Score	DB 1	Length	DB 2	Score	DB 3	Length	DB 4	Score	DB 5	Length	DB 6	Score	DB 7	Length	DB 8	Score	DB 9	Length	DB 10	Score	DB 11	Length	DB 12	Score	DB 13	Length	DB 14	Score	DB 15	Length	DB 16	Score	DB 17	Length	DB 18	Score	DB 19	Length	DB 20	Score	DB 21	Length	DB 22	Score	DB 23	Length	DB 24	Score	DB 25	Length	DB 26	Score	DB 27	Length	DB 28	Score	DB 29	Length	DB 30	Score	DB 31	Length	DB 32	Score	DB 33	Length	DB 34	Score	DB 35	Length	DB 36	Score	DB 37	Length	DB 38	Score	DB 39	Length	DB 40	Score	DB 41	Length	DB 42	Score	DB 43	Length	DB 44	Score	DB 45	Length	DB 46	Score	DB 47	Length	DB 48	Score	DB 49	Length	DB 50	Score	DB 51	Length	DB 52	Score	DB 53	Length	DB 54	Score	DB 55	Length	DB 56	Score	DB 57	Length	DB 58	Score	DB 59	Length	DB 60	Score	DB 61	Length	DB 62	Score	DB 63	Length	DB 64	Score	DB 65	Length	DB 66	Score	DB 67	Length	DB 68	Score	DB 69	Length	DB 70	Score	DB 71	Length	DB 72	Score	DB 73	Length	DB 74	Score	DB 75	Length	DB 76	Score	DB 77	Length	DB 78	Score	DB 79	Length	DB 80	Score	DB 81	Length	DB 82	Score	DB 83	Length	DB 84	Score	DB 85	Length	DB 86	Score	DB 87	Length	DB 88	Score	DB 89	Length	DB 90	Score	DB 91	Length	DB 92	Score	DB 93	Length	DB 94	Score	DB 95	Length	DB 96	Score	DB 97	Length	DB 98	Score	DB 99	Length	DB 100	Score	DB 101	Length	DB 102	Score	DB 103	Length	DB 104	Score	DB 105	Length	DB 106	Score	DB 107	Length	DB 108	Score	DB 109	Length	DB 110	Score	DB 111	Length	DB 112	Score	DB 113	Length	DB 114	Score	DB 115	Length	DB 116	Score	DB 117	Length	DB 118	Score	DB 119	Length	DB 120	Score	DB 121	Length	DB 122	Score	DB 123	Length	DB 124	Score	DB 125	Length	DB 126	Score	DB 127	Length	DB 128	Score	DB 129	Length	DB 130	Score	DB 131	Length	DB 132	Score	DB 133	Length	DB 134	Score	DB 135	Length	DB 136	Score	DB 137	Length	DB 138	Score	DB 139	Length	DB 140	Score	DB 141	Length	DB 142	Score	DB 143	Length	DB 144	Score	DB 145	Length	DB 146	Score	DB 147	Length	DB 148	Score	DB 149	Length	DB 150	Score	DB 151	Length	DB 152	Score	DB 153	Length	DB 154	Score	DB 155	Length	DB 156	Score	DB 157	Length	DB 158	Score	DB 159	Length	DB 160	Score	DB 161	Length	DB 162	Score	DB 163	Length	DB 164	Score	DB 165	Length	DB 166	Score	DB 167	Length	DB 168	Score	DB 169	Length	DB 170	Score	DB 171	Length	DB 172	Score	DB 173	Length	DB 174	Score	DB 175	Length	DB 176	Score	DB 177	Length	DB 178	Score	DB 179	Length	DB 180	Score	DB 181	Length	DB 182	Score	DB 183	Length	DB 184	Score	DB 185	Length	DB 186	Score	DB 187	Length	DB 188	Score	DB 189	Length	DB 190	Score	DB 191	Length	DB 192	Score	DB 193	Length	DB 194	Score	DB 195	Length	DB 196	Score	DB 197	Length	DB 198	Score	DB 199	Length	DB 200	Score	DB 201	Length	DB 202	Score	DB 203	Length	DB 204	Score	DB 205	Length	DB 206	Score	DB 207	Length	DB 208	Score	DB 209	Length	DB 210	Score	DB 211	Length	DB 212	Score	DB 213	Length	DB 214	Score	DB 215	Length	DB 216	Score	DB 217	Length	DB 218	Score	DB 219	Length	DB 220	Score	DB 221	Length	DB 222	Score	DB 223	Length	DB 224	Score	DB 225	Length	DB 226	Score	DB 227	Length	DB 228	Score	DB 229	Length	DB 230	Score	DB 231	Length	DB 232	Score	DB 233	Length	DB 234	Score	DB 235	Length	DB 236	Score	DB 237	Length	DB 238	Score	DB 239	Length	DB 240	Score	DB 241	Length	DB 242	Score	DB 243	Length	DB 244	Score	DB 245	Length	DB 246	Score	DB 247	Length	DB 248	Score	DB 249	Length	DB 250	Score	DB 251	Length	DB 252	Score	DB 253	Length	DB 254	Score	DB 255	Length	DB 256	Score	DB 257	Length	DB 258	Score	DB 259	Length	DB 260	Score
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Query Match	100.0%;	Score 27;	DB 6;	Length 1032;
Best Local Similarity	100.0%;	Pred. No. 0.51;		
Matches 27;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 CCTATCCTGTTTGTGTTAAGCCGCGC 27			
Db	494 CCTATCCTGTTTGTGTTAAGCCGCGC 520			
RESULT 9				
LOCUS	CQ797595	1034 bp	DNA	linear PAT 20-APR-2004
DEFINITION	Sequence 9 from Patent EP1408120.			
ACCESSION	CQ797595			
VERSION	CQ797595.1	GI:46425867		
KEYWORDS				
SOURCE	Enterococcus faecium			
ORGANISM	Enterococcus faecium			
REFERENCE	1			
AUTHORS	Cockerill, P. R. and Sloan, L. M.			
TITLE	Detection of vancomycin-resistant Enterococcus spp			
JOURNAL	Patent: EP 1408120-A 9 14-APR-2004;			
FEATURES	MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)			
source	location/Qualifiers			
ORIGIN	1..1034			
	/organism="Enterococcus faecium"			
	/mol_type="unassigned DNA"			
	/db_xref="taxon:1352"			
Query Match	100.0%;	Score 27;	DB 6;	Length 1034;
Best Local Similarity	100.0%;	Pred. No. 0.51;		
Matches 27;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 CCTATCCTGTTTGTGTTAAGCCGCGC 27			
Db	494 CCTATCCTGTTTGTGTTAAGCCGCGC 520			
RESULT 10				
LOCUS	AX110322	1218 bp	DNA	linear PAT 29-MAY-2002
DEFINITION	Sequence 1055 from Patent WO0123604.			
ACCESSION	AX110322			
VERSION	AX110322.1	GI:13926614		
KEYWORDS				
SOURCE	Enterococcus gallinarum			
ORGANISM	Enterococcus gallinarum			
REFERENCE	1			
AUTHORS	Bergeron, M. G., Boiesnot, M., Huletsky, A., m Nard, C., Ouellette, M.,			
TITLE	Picard, P. J., and Roy, P. H.			
JOURNAL	Highly conserved genes and their use to generate probes and primers			
FEATURES	for detection of microorganisms			
source	Patent: WO 0123604-A 1055 05-APR-2001;			
	Infectio Diagnostic (I.D.I.) INC. (CA)			
	location/Qualifiers			
	1..1218			
	/organism="Enterococcus gallinarum"			
	/mol_type="unassigned DNA"			
	/strain="R684"			
	/db_xref="taxon:1353"			

Query Match 100.0%; Score 27; DB 6; Length 1218;
 Best Local Similarity 100.0%; Pred. No. 0.5;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
 Db 568 CCTATCCTGTTTGTGTAAGCGGCGC 594

RESULT 11
 AX110321 1232 bp DNA linear PAT 29-MAY-2002
 LOCUS Sequence 1054 from Patent WO0123604.
 DEFINITION AX110321
 ACCESSION AX110321
 VERSION AX110321.1 GI:13926613
 KEYWORDS Enterococcus faecalis
 SOURCE Enterococcus faecalis
 ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
 Enterococcus.

REFERENCE 1
 AUTHORS Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
 Picard, P.J. and Roy, P.H.
 TITLE Highly conserved genes and their use to generate probes and primers
 JOURNAL for detection of microorganisms
 PATENT: WO 0123604-A 1054 05-APR-2001;
 Infectio Diagnostic (I.D.I.) INC. (CA)
 FEATURES Location/Qualifiers
 source 1..1232
 /organism="Enterococcus faecalis"
 /mol_type="unassigned DNA"
 /db_xref="taxon:1351"
 /note="R610"

ORIGIN
 Query Match 100.0%; Score 27; DB 6; Length 1232;
 Best Local Similarity 100.0%; Pred. No. 0.5;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
 Db 578 CCTATCCTGTTTGTGTAAGCGGCGC 604

RESULT 12
 AX110319 1237 bp DNA linear PAT 29-MAY-2002
 LOCUS Sequence 1052 from Patent WO0123604.
 DEFINITION AX110319
 ACCESSION AX110319
 VERSION AX110319.1 GI:13926611
 KEYWORDS Enterococcus faecium
 SOURCE Enterococcus faecium
 ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
 Enterococcus.

REFERENCE 1
 AUTHORS Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
 Picard, P.J. and Roy, P.H.
 TITLE Highly conserved genes and their use to generate probes and primers
 JOURNAL for detection of microorganisms
 PATENT: WO 0123604-A 1052 05-APR-2001;
 Infectio Diagnostic (I.D.I.) INC. (CA)
 FEATURES Location/Qualifiers
 source 1..1237
 /organism="Enterococcus faecium"
 /mol_type="unassigned DNA"
 /strain="R492"
 /db_xref="taxon:1352"

ORIGIN
 Query Match 100.0%; Score 27; DB 6; Length 1237;
 Best Local Similarity 100.0%; Pred. No. 0.5;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
 Db 590 CCTATCCTGTTTGTGTAAGCGGCGC 616

RESULT 13
 AX110316 1241 bp DNA linear PAT 29-MAY-2002
 LOCUS Sequence 1049 from Patent WO0123604.
 DEFINITION AX110316
 ACCESSION AX110316
 VERSION AX110316.1 GI:13926608
 KEYWORDS Enterococcus faecium
 SOURCE Enterococcus faecium
 ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
 Enterococcus.

REFERENCE 1
 AUTHORS Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
 Picard, P.J. and Roy, P.H.
 TITLE Highly conserved genes and their use to generate probes and primers
 JOURNAL for detection of microorganisms
 PATENT: WO 0123604-A 1049 05-APR-2001;
 Infectio Diagnostic (I.D.I.) INC. (CA)
 FEATURES Location/Qualifiers
 source 1..1241
 /organism="Enterococcus faecium"
 /mol_type="unassigned DNA"
 /strain="R690"
 /db_xref="taxon:1352"

ORIGIN
 Query Match 100.0%; Score 27; DB 6; Length 1241;
 Best Local Similarity 100.0%; Pred. No. 0.5;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
 Db 561 CCTATCCTGTTTGTGTAAGCGGCGC 587

RESULT 14
 AX110317 1249 bp DNA linear PAT 29-MAY-2002
 LOCUS Sequence 1050 from Patent WO0123604.
 DEFINITION AX110317
 ACCESSION AX110317
 VERSION AX110317.1 GI:13926609
 KEYWORDS Enterococcus gallinarum
 SOURCE Enterococcus gallinarum
 ORGANISM Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
 Enterococcus.

REFERENCE 1
 AUTHORS Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
 Picard, P.J. and Roy, P.H.
 TITLE Highly conserved genes and their use to generate probes and primers
 JOURNAL for detection of microorganisms
 PATENT: WO 0123604-A 1050 05-APR-2001;
 Infectio Diagnostic (I.D.I.) INC. (CA)
 FEATURES Location/Qualifiers
 source 1..1249
 /organism="Enterococcus gallinarum"
 /mol_type="unassigned DNA"
 /strain="R691"
 /db_xref="taxon:1353"

ORIGIN
 Query Match 100.0%; Score 27; DB 6; Length 1249;
 Best Local Similarity 100.0%; Pred. No. 0.5;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTGTAAGCGGCGC 27

Db 590 CCTATCCTGTTTGTAAAGCCGGCGC 616

RESULT 15
LOCUS AX110320 1263 bp DNA linear PAT 29-MAY-2002
DEFINITION Sequence 1053 from Patent WO0123604.
ACCESSION AX110320
VERSION AX110320.1 GI:13926612
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE
AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
JOURNAL for detection of microorganisms
PATENT: WO 0123604-A 1053 05-APR-2001;
INfectio Diagnostic (I.D.I.) INC. (CA)
FEATURES
Source Location/Qualifiers
1. .1263
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/strain="R581"
/db_xref="taxon:1352"

ORIGIN
Query Match 100.0%; Score 27; DB 6; Length 1263;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTAAAGCCGGCGC 27
|||||
Db 582 CCTATCCTGTTTGTAAAGCCGGCGC 608
|||||

RESULT 16
LOCUS AX110323 1265 bp DNA linear PAT 29-MAY-2002
DEFINITION Sequence 1056 from Patent WO0123604.
ACCESSION AX110323
VERSION AX110323.1 GI:13926615
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE
AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
JOURNAL for detection of microorganisms
PATENT: WO 0123604-A 1056 05-APR-2001;
INfectio Diagnostic (I.D.I.) INC. (CA)
FEATURES
Source Location/Qualifiers
1. .1265
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/strain="R688"
/db_xref="taxon:1352"

ORIGIN
Query Match 100.0%; Score 27; DB 6; Length 1265;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTAAAGCCGGCGC 27
|||||
Db 592 CCTATCCTGTTTGTAAAGCCGGCGC 618
|||||

RESULT 17
LOCUS AX110324 1269 bp DNA linear PAT 29-MAY-2002
DEFINITION Sequence 1057 from Patent WO0123604.
ACCESSION AX110324
VERSION AX110324.1 GI:13926616
KEYWORDS
SOURCE Enterococcus flavescens
ORGANISM Enterococcus flavescens
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE
AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
JOURNAL for detection of microorganisms
PATENT: WO 0123604-A 1057 05-APR-2001;
INfectio Diagnostic (I.D.I.) INC. (CA)
FEATURES
Source Location/Qualifiers
1. .1269
/organism="Enterococcus flavescens"
/mol_type="unassigned DNA"
/strain="R689"
/db_xref="taxon:37735"

ORIGIN
Query Match 100.0%; Score 27; DB 6; Length 1269;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTAAAGCCGGCGC 27
|||||
Db 590 CCTATCCTGTTTGTAAAGCCGGCGC 616
|||||

RESULT 18
LOCUS AX110318 1272 bp DNA linear PAT 29-MAY-2002
DEFINITION Sequence 1051 from Patent WO0123604.
ACCESSION AX110318
VERSION AX110318.1 GI:13926610
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE
AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
JOURNAL for detection of microorganisms
PATENT: WO 0123604-A 1051 05-APR-2001;
INfectio Diagnostic (I.D.I.) INC. (CA)
FEATURES
Source Location/Qualifiers
1. .1272
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/strain="R481"
/db_xref="taxon:1352"

ORIGIN
Query Match 100.0%; Score 27; DB 6; Length 1272;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTAAAGCCGGCGC 27
|||||
Db 570 CCTATCCTGTTTGTAAAGCCGGCGC 596
|||||

RESULT 19
LOCUS EFPVANAG 1768 bp DNA linear BCT 17-JUN-1991

DEFINITION B.faecium plasmid p1816 vana gene for VANA ligase.
 ACCESSION X56895
 VERSION X56895.1 GI:43335
 KEYWORDS D-alanyl-D-alanine ligase; VANA glycopeptide resistance protein;
 vancomycin resistance.
 SOURCE Enterococcus faecium
 ORGANISM Enterococcus faecium
 Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
 Enterococcus.
 REFERENCE 1 (bases 1 to 1768)
 AUTHORS Dutka-Malen, S., Molinas, C., Arthur, M. and Courvalin, P.
 TITLE The VANA glycopeptide resistance protein is related to
 D-alanyl-D-alanine ligase cell wall biosynthesis enzymes
 JOURNAL Mol. Gen. Genet. 224 (3), 364-372 (1990)
 PUBMED 2266943
 REFERENCE 2 (bases 1 to 1768)
 AUTHORS Dutka-Malen, S.
 TITLE Direct Submission
 JOURNAL Submitted (25-FEB-1991) S. Dutka-Malen, Institut Pasteur, Uille des
 Agents Antibacteriens, 28 rue du Dr Roux, Paris Cedex 15, France
 FEATURES
 source
 1.1768
 /organism="Enterococcus faecium"
 /mol_type="genomic DNA"
 /strain="BM4147"
 /db_xref="taxon:1352"
 /plasmid="p1816"
 360..369
 377..1408
 /gene="vana"
 377..1408
 /gene="vana"
 377..1408
 /gene="vana"
 /codon_start=1
 /evidence=experimental
 /transl_table=11
 /product="VANA ligase"
 /protein_id="CAA40215.1"
 /db_xref="GI:43336"
 /db_xref="GOA:P25051"
 /db_xref="UniProt/Swiss-Prot:P25051"
 /translation="MNRIVKALIFGCGSEHDVVKAIHIANINKEKTEPIYIT
 KSGVMTCRCPAEWENDCYSAVSPKRNKGLVKNHREINHYDVAFSLHRS
 GEGSIOGLFELSGIPVGCIDQSALICMDSLTYIAKXNAGIATPAFWINDDPV
 AATFYTPVKPARSGSGSGYKVKNSADELDYALISARQDSKLLLEAVSGCEVCA
 VIGNSALVAVGVDQIRLOYGIFRIHSEVBEKSENAVITVPADLSAERGIQETA
 KIKVRLGCGRLARVDMRLQDNGRIVLNVTLLGFTSYSRIPPMMAAGIALPELID
 RLIVLAKG"

ORIGIN
 Query Match 100.0%; Score 27; DB 1; Length 1768;
 Best Local Similarity 100.0%; Pred. No. 0.48;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
 Db 870 CCTATCCTGTTTGTGTAAGCCGCGC 896

RESULT 20
 LOCUS CQ797596 1768 bp DNA linear PAT 20-APR-2004
 DEFINITION Sequence 10 from Patent EP1408120.
 ACCESSION CQ797596
 VERSION CQ797596.1 GI:46425888
 KEYWORDS Enterococcus faecium
 SOURCE Enterococcus faecium
 ORGANISM Enterococcus faecium
 Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
 Enterococcus.
 REFERENCE 1
 AUTHORS Cockerill, F.R. and Sloan, L.M.
 TITLE Detection of vancomycin-resistant Enterococcus spp
 JOURNAL Patent: EP 1408120-A 10 14-APR-2004;

FEATURES
 source
 1.1768
 /organism="Enterococcus faecium"
 /mol_type="unassigned DNA"
 /db_xref="taxon:1352"
 /note="vana sequence"

ORIGIN
 Query Match 100.0%; Score 27; DB 6; Length 1768;
 Best Local Similarity 100.0%; Pred. No. 0.48;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
 Db 870 CCTATCCTGTTTGTGTAAGCCGCGC 896

RESULT 21
 LOCUS CQ797597 1768 bp DNA linear PAT 20-APR-2004
 DEFINITION Sequence 11 from Patent EP1408120.
 ACCESSION CQ797597
 VERSION CQ797597.1 GI:46425889
 KEYWORDS Enterococcus faecium
 SOURCE Enterococcus faecium
 ORGANISM Enterococcus faecium
 Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
 Enterococcus.
 REFERENCE 1
 AUTHORS Cockerill, F.R. and Sloan, L.M.
 TITLE Detection of vancomycin-resistant Enterococcus spp
 JOURNAL Patent: EP 1408120-A 11 14-APR-2004;
 MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
 FEATURES
 source
 1.1768
 /organism="Enterococcus faecium"
 /mol_type="unassigned DNA"
 /db_xref="taxon:1352"
 /note="vana sequence"

ORIGIN
 Query Match 100.0%; Score 27; DB 6; Length 1768;
 Best Local Similarity 100.0%; Pred. No. 0.48;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
 Db 870 CCTATCCTGTTTGTGTAAGCCGCGC 896

RESULT 22
 LOCUS CS061873 1768 bp DNA linear PAT 13-APR-2005
 DEFINITION Sequence 1 from Patent WO2005028679.
 ACCESSION CS061873
 VERSION CS061873.1 GI:62553767
 KEYWORDS Enterococcus faecium
 SOURCE Enterococcus faecium
 ORGANISM Enterococcus faecium
 Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
 Enterococcus.
 REFERENCE 1
 AUTHORS Dodgson, K.J.
 TITLE Method and kit for identifying vancomycin-resistant enterococcus
 JOURNAL Patent: WO 2005028679-A 1 31-MAR-2005;
 University of Iowa Research Foundation (US); DODGSON, Kirsty Jane
 (US)
 FEATURES
 source
 1.1768
 /organism="Enterococcus faecium"
 /mol_type="unassigned DNA"
 /db_xref="taxon:1352"

ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 1768;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTGTTAAGCCGCGC 27
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Db 870 CCTATCCTGTTTGTGTTAAGCCGCGC 896

RESULT 23
AX110406 1768 bp DNA linear PAT 29-MAY-2002
LOCUS Sequence 1139 from Patent WO0123604.
DEFINITION AX110406
ACCESSION AX110406.1 GI:13926698
VERSION
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE 1
AUTHORS Bergeron,M.G., Bolesinc,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
JOURNAL Patent: WO 0123604-A 1139 05-APR-2001;
FEATURES Infectio Diagnostic (I.D.I.) INC. (CA)
source Location/Qualifiers
1. 1768
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/strain="BM4147"
/db_xref="taxon:1352"

ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 1768;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTGTTAAGCCGCGC 27
|||||
Db 870 CCTATCCTGTTTGTGTTAAGCCGCGC 896

RESULT 24
AR089411 2607 bp DNA linear PAT 07-SEP-2000
LOCUS AR089411
DEFINITION Sequence 170 from patent US 5994066.
ACCESSION AR089411
VERSION AR089411.1 GI:10016168
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2607)
AUTHORS Bergeron,M.G., Picard,F.J., Ouellette,M. and Roy,P.H.
TITLE Species-specific and universal DNA probes and amplification primers
to rapidly detect and identify common bacterial pathogens and
associated antibiotic resistance genes from clinical specimens for
routine diagnosis in microbiology laboratories
JOURNAL Patent: US 5994066-A 170 30-NOV-1999;
FEATURES Location/Qualifiers
1. 2607
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 2607;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTGTTAAGCCGCGC 27
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Db 1455 CCTATCCTGTTTGTGTTAAGCCGCGC 1481

RESULT 25
AR093611 2607 bp DNA linear PAT 08-SEP-2000
LOCUS AR093611
DEFINITION Sequence 170 from patent US 6001564.
ACCESSION AR093611
VERSION AR093611.1 GI:10020360
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2607)
AUTHORS Bergeron,M.G., Ouellette,M. and Roy,P.H.
TITLE Species specific and universal DNA probes and amplification primers
to rapidly detect and identify common bacterial pathogens and
associated antibiotic resistance genes from clinical specimens for
routine diagnosis in microbiology laboratories
JOURNAL Patent: US 6001564-A 170 14-DEC-1999;
FEATURES Location/Qualifiers
1. 2607
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 2607;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTGTTAAGCCGCGC 27
|||||
Db 1455 CCTATCCTGTTTGTGTTAAGCCGCGC 1481

RESULT 26
AR035514 2667 bp DNA linear PAT 29-SEP-1999
LOCUS AR035514
DEFINITION Sequence 17 from patent US 5871910.
ACCESSION AR035514
VERSION AR035514.1 GI:5952182
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2667)
AUTHORS Arthur,M., Dutka-Mallen,S., Molina,C. and Courvalin,P.
TITLE Probes for the detection of nucleotide sequences implicated in the
expression of resistance to glycopeptides, in particular in
gram-positive bacteria
JOURNAL Patent: US 5871910-A 17 16-FEB-1999;
FEATURES Location/Qualifiers
1. 2667
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 2667;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCCTGTTTGTGTTAAGCCGCGC 27
|||||
Db 1518 CCTATCCTGTTTGTGTTAAGCCGCGC 1544

RESULT 27
BD181855 2667 bp DNA linear PAT 15-MAY-2003
LOCUS BD181855
DEFINITION Polypeptides implicated in the expression of resistance to
glycopeptides, in particular in gram-positive bacteria, nucleotide

sequence coding for these polypeptides and use for diagnosis.

ACCESSION BD181855
VERSION JP 2002320494-A/11
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified

REFERENCE 1 (bases 1 to 2667)
AUTHORS Arthur, M., Duktamalen, S., Molinas, C. and Courvalin, P.
TITLE Polypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nucleotide sequence coding for these polypeptides and use for diagnosis
JOURNAL Patent: JP 2002320494-A 11 05-NOV-2002;
INSTITUT PASTEUR
COMMENT OS Bacteria
PN JP 2002320494-A/11
PD 05-NOV-2002
PP 21-FEB-2002 JP 2002045484
PR 31-OCT-1990 FR 90/13579
PI MICHEL, ARTHUR, SYLVIE DUKTA-MALEN, CATHERINE MOLINAS, PATRICE PI COURVALIN
PC C12N15/09, C07K14/315, C07K16/12, C12N1/15, C12N1/19, C12N1/21, PC C12N5/10,
PC C12Q1/04, C12Q1/68, G01N33/53, G01N33/566, G01N33/569//C12P21/08, PC (C12Q1/04, C12R1:01), (C12Q1/68, C12R1:01), C12N15/00, C12N5/00 CC
Polypeptides implicated in the expression of resistance to CC glycopeptides, in particular in gram-positive bacteria, nucleotide sequence coding for these polypeptides and use for diagnosis
CC in particular in gram-positive bacteria, nucleotide sequence coding for these polypeptides and use for diagnosis
CC Key Location/Qualifiers
FT source 1.2667
FEATURES source 1.2667
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 2667;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCGTGTGTTGTTAAGCCGCGC 27
|||||
Db 1518 CCTATCGTGTGTTGTTAAGCCGCGC 1544

RESULT 28
AX110408 3946 bp DNA linear PAT 29-MAY-2002
LOCUS Sequence 1141 from Patent WO0123604.
DEFINITION AX110408
ACCESSION AX110408
VERSION AX110408.1 GI:13926700
KEYWORDS Enterococcus faecium
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

REFERENCE 1
AUTHORS Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M., Picaud, F.J. and Roy, P.H.
TITLE Highly conserved genes and their use to generate probes and primers for detection of microorganisms
JOURNAL Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES source 1.3946
/organism="Enterococcus faecium"
/mol_type="unassigned DNA"
/strain="BM4147"
/db_xref="taxon:1352"

ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 3946;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTATCGTGTGTTGTTAAGCCGCGC 27
|||||
Db 1455 CCTATCGTGTGTTGTTAAGCCGCGC 1481

RESULT 29
AY926880 4654 bp DNA linear BCT 06-MAR-2005
LOCUS Paenibacillus thiaminolyticus R3A1221 vana resistance gene cluster, complete sequence.
DEFINITION AY926880
ACCESSION AY926880
VERSION AY926880.1 GI:60391954
KEYWORDS Paenibacillus thiaminolyticus
SOURCE Paenibacillus thiaminolyticus
ORGANISM Paenibacillus thiaminolyticus
Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
REFERENCE 1 (bases 1 to 4654)
AUTHORS Moodley, A., van Niekerk, W. and Marais, B.
TITLE Paenibacillus thiaminolyticus R3A1221 vana resistance gene cluster unpublished
JOURNAL 2 (bases 1 to 4654)
AUTHORS Moodley, A., van Niekerk, W. and Marais, B.
TITLE Direct Submission
JOURNAL Submitted (10-FEB-2005) Clinical Microbiology and Infectious Diseases, University of the Witwatersrand, 7 York Road, Parktown, Johannesburg, Gauteng 2193, South Africa
FEATURES source 1.4654
/organism="Paenibacillus thiaminolyticus"
/mol_type="genomic DNA"
/strain="R3A1221"
/db_xref="taxon:49283"
1.696
/gene="vanR"
1.696
/gene="vanR"
/codon_start=1
/trna1_table=1
/product="transcriptional response regulator"
/protein_id="AA19281.1"
/db_xref="GI:60391955"
/translation="MSDKILIVDDSHBIADIVELVLYKNENYVFKYATKALAECDK SEIDIAIDIMLPSTSGLTICOKIRDKHTYPIMLTGQREVQDTGLTIGADYITK PPRFELIARVKAQLRRYKFSGVKQSENVIVHSGLVINVTRECYLNEKQSLATP EFSILRLICENKGVSSSLPFIIMWDEYFSKSNNTITVAIRLRKMDTIDNPKY IKTVWGYYKIEK"
674.1834
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674.1834
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/codon_start=1
/trna1_table=1
/product="thiolidase protein kinase"
/protein_id="AA19282.1"
/db_xref="GI:60391956"
/translation="MAIKIKNNKKTKDYSKLRKLYOYIVYVMAAVFVFLPLFLTK GLGEMIVRFLNSYHLDLDMKLYOYSINNDIFVYAVISILICRWLMSKPA KYRDBINIGDVIDIONEKOIELSAMWEOCKNTLKRLEKQDAKLABRKNDV VMLADITPLPISIIIGTSLDEAPDMPVDQAKTVHTLDKAVRLBQULDFEFT RYMLQTTTLTKHIDLTYMLVQMTDEFYQSLASGKQAVIHABEDTLVSGDPKLRV FNNILBAAYSESDNSVIDITAGSGDVASIVFKNAGSIPDKLAAIPEKFTYLDQAR SSPDGGAGLAIKAEIIVQHGCGIVASNSNNTTFTVBLPALPDLVDRKSS"
2048.3016
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/gene="vanH"
/codon_start=1

/trna1 table=11
/product="D-specific dehydrogenase"
/protein_id="AA19283.1"
/db_xref="GI:60391957"
/translation="MANNIGITVYGCEDDADFALSPRGWPSIINAVSRSNKS
APFNQISVGHKEVSASITLALRKAGVKITSTRSGCNHIDTTAKRKGITVGNAY
SPDSVADYTMMLMVAVRNKSIVRSVEKIDFRLDSVRGVLSDMTVGAVGTHIKA
VIERLRGFGCKVLARSOSIENAVYFPDELQNSDIVTLLHPLNADTHIISHEQIO
RMKOGAFIINTGRLPYTNELVKALENGGAALDVGEEEPFYSQSPKIDNO
FLIKQRMVVIITTPHTAFYTBQALRDYTKNKINCLDFRSGEHE"
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/codon_start=1
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/product="D-alanine-D-lactate ligase"
/protein_id="AA19284.1"
/db_xref="GI:60391958"
/translation="MNRVKYAILFGGCEBHDVSVKAREIANINDEKYEPLYGIT
KSGVMKCEKPECAEMENSNCYSAVLSPDKHQGLVKNHEVYIHHVDVAFSGMSKS
GEGSIQGLFELSGIPVCGDIOSSAICMDKSLTYTAKNAGIAIDPEFWINDDPA
ADPTTPVFKPKPARSGSSYGVKYNVADDEDAIBSRKQYDSKILIRQAVLCEVCA
VLNSSLIVGEVDQIRLQGITFRIHQEAPEKSENAVITIPADLSAERKIQETA
KKIYKALGCRGLRVDMFLQDNGRIVLNEVNTLPGFTYSRYPRMMAAAGITLPELID
RLIVPALQG"
4046..4654
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/gene="vanX"
/codon_start=1
/trna1 table=11
/product="D,D-dipeptidase"
/protein_id="AA19285.1"
/db_xref="GI:60391959"
/translation="MKKGFTFLBEILHGVMDAKATATDNFPGKPDVGEVNFIACTY
ELADALIKVELAAQGYGLLDGYRQRAVNCFYQMAQPDGLTKERYYNIRRT
EMYSKGVASKSSHSRGSALDTLRYDTGELVPMGSGFPMERSHHAKGISGMEA
QNRCLRSINENSGFEAYSEFWMHYVLRNPFYNSYDFPVK"
ORIGIN
Query Match 100.0%; Score 27; DB 1; Length 4654;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
Db 3502 CCTATCCTGTTTGTGTAAGCGGCGC 3528
RESULT 30
AR035512
LOCUS AR035512 7225 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 15 from patent US 5871910.
ACCESSION AR035512
VERSION AR035512.1 GI:5952180
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 7225)
Arthur,M., Dukta-Malen,S., Molinas,C. and Courvalin,P.
Probes for the detection of nucleotide sequences implicated in the
expression of resistance to glycopeptides, in particular in
gram-positive bacteria
Patent: US 5871910-A 15 FEB-1999;
location/Qualifiers
1..7225
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 27; DB 6; Length 7225;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
Db 5016 CCTATCCTGTTTGTGTAAGCGGCGC 5042

Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
Db 5016 CCTATCCTGTTTGTGTAAGCGGCGC 5042
RESULT 31
BD181853
LOCUS BD181853 7225 bp DNA linear PAT 15-MAY-2003
DEFINITION Polypeptides implicated in the expression of resistance to
glycopeptides, in particular in gram-positive bacteria, nucleotide
sequence cod ing for these polypeptides and use for diagnosis.
ACCESSION BD181853
VERSION BD181853.1 GI:30792771
KEYWORDS JP 2002320494-A/9.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 7225)
Arthur,M., Duktemalen,S., Molinas,C. and Courvalin,P.
Polypeptides implicated in the expression of resistance to
glycopeptides, in particular in gram-positive bacteria, nucleotide
sequence cod ing for these polypeptides and use for diagnosis
Patent: JP 2002320494-A 9 05-NOV-2002;
INSTITUT PASTEUR
OS Bacteria
PN JP 2002320494-A/9
PD 05-NOV-2002 JP 2002045484
PF 21-FEB-2002 JP 2002045484
PR 31-OCT-1990 FR 90/13579
PI MICHEL ARTHUR, SYLVIE DUKTA-MALEN, CATHERINE MOLINAS, PATRICE PI
COURVALIN
PC C12N15/09, C07K14/315, C07K16/12, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10, C12Q1/04, C12Q1/68, G01N33/53, G01N33/566, G01N33/569, C12P21/08,
PC C12Q1/04, C12R1/01, C12Q1/68, C12R1/01, C12N15/00, C12N5/00 CC
Polypeptides implicated in the expression of resistance to CC
glycopeptides,
CC in particular in gram-positive bacteria, nucleotide sequence
cod ing for
CC these polypeptides and use for diagnosis
FH Key location/Qualifiers
FT source 1..7225
/organism="Bacteria".
FEATURES
source location/Qualifiers
1..7225
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 100.0%; Score 27; DB 6; Length 7225;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
Db 5016 CCTATCCTGTTTGTGTAAGCGGCGC 5042
RESULT 32
DQ018711
LOCUS DQ018711 9519 bp DNA linear BCT 31-MAY-2005
DEFINITION Paenibacillus apiarius strain Pa-B2B glycopeptide resistance vana
operon, complete sequence; and Btu-like protein gene, partial cds.
ACCESSION DQ018711
VERSION DQ018711.1 GI:66731642
KEYWORDS
SOURCE Paenibacillus apiarius
ORGANISM Paenibacillus apiarius
Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.

REFERENCE 1 (bases 1 to 9519)
AUTHORS Guardabassi, L., Perichon, B., Van Heijenoort, J., Blanot, D. and Courvalin, P.
TITLE Glycopeptide resistance van operons in *Paenibacillus* from soil
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 9519)
AUTHORS Guardabassi, L., Perichon, B., Van Heijenoort, J., Blanot, D. and Courvalin, P.
TITLE Direct Submission
JOURNAL Submitted (26-Apr-2005) Unite des Agents Antibacteriens, Institut Pasteur, 25 rue du Docteur Roux, Paris 75015, France
FEATURES
source
1. 9519
/organism="Paenibacillus ariarius"
/mol_type="genomic DNA"
/strain="PA-B2B"
/isolation_source="soil"
/db_xref="taxon:46240"
1. 7648
/operon="glycopeptide resistance vanA"
1. 696
/gene="vanR"
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1. 696
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/operon="glycopeptide resistance vanA"
/note="response regulator"
/codon_start=1
/transl_table=1
/product="VanR"
/protein_id="AAV52009.1"
/db_xref="GI:66731643"
/translation="MSDKILVDDDEHIDLYELVYKNNENTVETKYTAKALECIDK
TDLDAIADIMLPGASGLAIQKIRDRHTVPIITLPAQOTEDVKITGLITADADYIRK
PFRPELTAIAQALRYKKNYGEQNEENVIVHSGLVININTECPLENEQLSLTPT
EESILRICENKGNVSSSEQLFRIWGDVFSNNNTIVHILREKMGNTIDNPKY
IKTWGCVGKTEK"
674. 1840
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/product="Vans"
/protein_id="AAV52010.1"
/db_xref="GI:66731644"
/translation="MAIKLNKKKKKKTKDYSKLRRLVOYIVIVMAAVPLRLRF
IKTIGEWIVAFLENSYHLERODAMIIYOTIRNNIEPIYVAIAISILICRWLSK
PAKYFDEINTGIDILIONEDKQIELSAEMSPBOKLNTKTLEREGDAGLAQRN
DVWYLAHDIKTPITSVIGYLSLIDEPAPMPVQAKYVHITLDAVYLBQIDEPF
ITRVMLQTTILTKKHIDLYLQMADEFPYPLAANGQAVIHASBDLTVGDSDKLA
RVFNMLLNAAVSEDSVIDITAGSGVSVIPEFGNSIPIKDLAIEKPEYRLD
AASSVTGAGIGLAIGIIVQGGQIVABSDNTTTPVEILPALPLVDKRS"
2047. 2862
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/product="VanH-like protein"
/protein_id="AAV52011.1"
/db_xref="GI:66731645"
/translation="MTQIPFPLPVVMQRKCFYAGKRFQGRVYATTDGKQLPYLT
FEAGALVNGKTVGDAVQENKVFNLAKLNLGLIRPGTSFRLVYADHAKHP
YKDGILVNGKLTAPAGGGLCOMSNLLFMWPLTPLVTRSGHVEKPEPPNDKIX
GVDAITSGWIDLKABNGTCTYQISVADPNDNIIGTVVDRKRGVLYRANGSIBRS
RESGIVBSVVERAIDSDTGBITQCKPLYNKCKICPLPENVEIKKAKV"
3168. 4136
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3168. 4136
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/operon="glycopeptide resistance vanA"
/note="dehydrogenase"
/codon_start=1
/transl_table=1
/product="VanH"
/protein_id="AAV52012.1"
/db_xref="GI:66731646"
/translation="MKNIQITITTCGQPDADVFKLSPPRGVLPATSSAVSTNNML
APNQCTISVGHKSEISSEILALKEGKVIKSTISIGNHIDMKAAESWGIANGVAY
SPDSVADYTLMLMAVNRKASIVASVEKDFKDSVGRGLDMVGTGVTGIGR
VIRLRGFGCHVLAIGHNKAANYVSNLELQSDILTHVPLSDVTGIMGRBQIK
AMEQGAFLNTARGGLIDIVLVYALRNGELGGAALVLEGSGLPYFCTQKPDNQ
FLNLQPMPEVITTPHTATTEQALRDVTVENTINCLEFRRRLV"
4129. 5160
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/operon="glycopeptide resistance vanA"
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/gene="vanA"
/operon="glycopeptide resistance vanA"
/note="D-Ala:D-Lac ligase"
/codon_start=1
/transl_table=1
/product="VanA"
/protein_id="AAV52016.1"
/db_xref="GI:66731650"
/translation="MYRVKIALIRGGCSREHDVSVKAKIANINTEKYEPIYIGIT
RSQVWCKEPCPDMDNRCASVLSPPKRRHGLVWRDGYQIQIIDAAPVYLHKS
GEGGAIQGLFELSGIPYGCDIQSSAVCMDSLAYIILAKNDGLATEPFWINDQRA
AAAFYVPEVKARSGSSYGVAKVGADELDAIARQYDSKILLEQVLGCEVCA
VLNSSELVIGVADQIRLOHGFIRHOBAPEKSENAVITIPADISAERGRIRTA
KIVYALGGKGLARVDMFLQDNGRIVANVTLPGLTSYSRPYRMVAAGITLPELID
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/operon="glycopeptide resistance vanA"
/note="D,D-di-peptidase"
/codon_start=1
/transl_table=1
/product="VanX"
/protein_id="AAV52017.1"
/db_xref="GI:66731651"
/translation="MEKGFVFLDLILGVWRDAKYATWDFNGKPYDGYENRIVGTH
AALALTKQKQAAALGYGLIMGYRPKAIVDCPLAWSQPDNITKERTYPINIBRT
EMVSKGVASKSHSRGSAIDLTLRLDTSELVPMGSGFDFDERSHHAAGIASMEA
QNRRLRSIMENSGEPYSPFWMYVILRNFTIQ"
6234. 7133
/gene="vanY"
/operon="glycopeptide resistance vanA"
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/gene="vanY"
/operon="glycopeptide resistance vanA"
/note="D,D-carboxypeptidase"
/codon_start=1
/transl_table=1
/product="VanY"
/protein_id="AAV52013.1"
/db_xref="GI:66731647"
/translation="MKKGFLLPLCLGAPINKALFQDKVEIQKTQNHKNIDN
IENIGPPLSIQNEIVKEQIYQSNLLINIKYPIRBSVSDIVNLSKNNELINQYL
LNTNITLSGLDQKFSSEMINDAVKGVSPFINSGRDPBQSVLYQEMGADVNLGAP
YSEHNSGLSDIVGSSSLTGERAPGKMLKENAKVGFILYPRDKTDVYGIQYBPMH
RYVGFPHSALMEKRNPALEXYMDPLKQKSIITTTIDHGYKIFPYVYISQNTTIPPAN
GQREISGNMDQVIYTVISGRD"
7169. 7648
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/operon="glycopeptide resistance vanA"

gene
CDS
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3168. 4136
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/codon_start=1
/transl_table=1
/product="VanH"
/protein_id="AAV52012.1"
/db_xref="GI:66731646"
/translation="MKNIQITITTCGQPDADVFKLSPPRGVLPATSSAVSTNNML
APNQCTISVGHKSEISSEILALKEGKVIKSTISIGNHIDMKAAESWGIANGVAY
SPDSVADYTLMLMAVNRKASIVASVEKDFKDSVGRGLDMVGTGVTGIGR
VIRLRGFGCHVLAIGHNKAANYVSNLELQSDILTHVPLSDVTGIMGRBQIK
AMEQGAFLNTARGGLIDIVLVYALRNGELGGAALVLEGSGLPYFCTQKPDNQ
FLNLQPMPEVITTPHTATTEQALRDVTVENTINCLEFRRRLV"
4129. 5160
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AAAFYVPEVKARSGSSYGVAKVGADELDAIARQYDSKILLEQVLGCEVCA
VLNSSELVIGVADQIRLOHGFIRHOBAPEKSENAVITIPADISAERGRIRTA
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6234. 7133
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8782..>9519
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ORIGIN
Query Match          100.0%; Score 27; DB 1; Length 9519;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 CCTATCCGTGTTTTGTTAACGCCGCGC 27
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Db       4622 CCTATCCGTGTTTTGTTAACGCCGCGC 4648

RESULT 33
LOCUS     DQ018710                9537 bp            linear   BCT 31-MAY-2005
DEFINITION Paenibacillus thiaminiolyticus strain PT-2B1 putative transposase
and putative GNAT family acetyltransferase genes, complete cds; and
glycopeptide resistance vana operon, partial sequence.
VERSION   DQ018710
KEYWORDS  DQ018710.1 GI:66731632
SOURCE    Paenibacillus thiaminiolyticus
ORGANISM  Paenibacillus thiaminiolyticus
REFERENCE 1 (bases 1 to 9537)
AUTHORS   Guardabassi,L., Perichon,B., Van Heijenoort,J., Blanot,D. and
Courvalin,P.
TITLE     Glycopeptide resistance van operons in Paenibacillus from soil
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 9537)
AUTHORS   Guardabassi,L., Perichon,B., Van Heijenoort,J., Blanot,D. and
Courvalin,P.
TITLE     Direct Submission
JOURNAL   Submitted (26-Apr-2005) Unite des Agents Antibacteriens, Institut
Pasteur, 25 rue du Docteur Roux, Paris 75015, France
FEATURES             Location/Qualifiers
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                     /protein_id="AAV52000.1"
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[illegible]

Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
Db 6563 CCTATCCTGTTTGTGTAAGCGGCGC 6569

RESULT 34
TRANVAN
LOCUS
DEFINITION
10851 bp DNA linear BCT 20-JUN-2002
Enterococcus faecium transposon Tn1546 transposase, resolvable, vanR
(vanR), vanS (vanS), vanH (vanH), vanX (vanX), vanY
(vanY), and telcoplanin resistance protein (vanZ) genes, complete
cds.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
M97297.1 GI:155036
Enterococcus faecium
Enterococcus faecium
Bacteria; Firmicutes; Lactobacilliales; Enterococcaceae;
Enterococcus.

REFERENCE
AUTHORS
TITLE
JOURNAL
PIRMBD
REFERENCES
JOURNAL
PIRMBD
FEATURES
SOURCE
1 (bases 1 to 10851)
Arthur M., Molinas C., Depardieu F. and Courvalin P.
Characterization of Tn1546, a Tn3-related transposon conferring
glycopeptide resistance by synthesis of depsipeptide peptidoglycan
precursors in Enterococcus faecium BM4147
J. Bacteriol. 175 (1), 117-127 (1993)
2 (bases 1 to 10851)
Arthur M., Depardieu F., Molinas C., Reynolds P. and Courvalin P.
The vanZ gene of Tn1546 from Enterococcus faecium BM4147 confers
resistance to telcoplanin
Gene 154 (1), 87-92 (1995)
7867956
Location/Qualifiers
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1. 10851
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1. 38
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SLAKTPTLRLVLEPHSTKANEPLQAVEIIRGNESGKRPVDSVPVDFISRWKRH
LVEDDQTTNRYHVMALVLELRHRAQGVISYGRQYDPFERYLPSBDTNQSKN
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KPSASLYOMLPRIKLTLDLMDVAHITGFHSGFTASNNRXPDKGRTIIMALLGGM
NIGLSMAATRGULTYKOLANVSGWRATEAMKAKAIIYNPRKQLQPRYMDGTS
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KLEALRQIQINIKVKENYEDVLAHSIBGVASLIMGKLSYSRQNSLATARE
MGIEKTIPIINYSIDSLRRIQIRGNKSGAMNGALRAIFPKQGLERLERTIQLOQ
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CDS
100.0%; Score 27; DB 1; Length 9537;
/codon_start=1

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IDAFTYFVFKPARSGSSGYKRVAGADELDALISARQYDSKILBOAVLGEVCA
VIGNSSELVGEVDQIRLQHGIFRIHDEAPEKSENAVITTPADLSVVRGRIQETA
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/db_xref="GI:66731640"
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SGSLDVGSSLTTERAPBGKMLKSNARKTIFILRYPKDKITVGTQYERPMHRIYGF
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Query Match

ORIGIN

gene	/translaction="MEIGFPLDEIVHGYRMDAKYATWMDFTCKPYDQGEVNIIVGTY ELASLILAKELAAATOGYGLIMDDGPRPRAVACFPMOAAQEPNNILTKSYVINIDRT EMISKGVASKSHSRGSAIDLTLYLDTGDELVPKMSRPDPFMRBSHHAANGISCNIEA QNRRLRSLIMENSGFEAYSLSEMHVYLRDEPYPNSYDFDPVK"			
CDS	9052..9963 /gene="vany" 9052..9963 /gene="vany" /codon_start=1 /transl_table=11 /protein_id="AA65958.1" /db_xref="GI:155044" /translaction="MKGLFLLILLFLIYLGVDYNEALFSQKVEFQYNDQPKETHL ENSGTSNTOEKTITEROYQGNLLILNSKYPYROBSYSDIYNLSKHDELINGGL DSNIYNSKEIAQKPFSEKNDYAKGVSHPIFINSGRYDPDQGSYLYQEMAEAYLAPGY SEHNSGLSDVGSLLTMEERAPKPKMIEENAMRYGFLIRPBDKTELGIQYBPWIR YVGIPEHAIKMEKNFLYEBRYADYLKSEKTISSVNBKXEIIFYPTKNTIIVPPTNL RYESGNNDGVIVTVPGSTHTNSRR"			
gene	10116..10601 /gene="varz" /gene="varz" 10116..10601 /gene="vanz" /codon_start=1 /transl_table=11 /product="telcoplanin resistance protein" /protein_id="AA65959.1" /db_xref="GI:801885" /translaction="MGRILSRGLALYVTLIWLVEKLQYILSVFNHQSLNLT PTANQFREMIDNVIIFIPGLILNVFKSIGFLPKPAFVLYLSFTBELLQIFALGA TDITDVTINTVGGPFLGKLXYGLSNKHNQKDLRVIIIFVGLILLVLLVYRTHLRINY V"			
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QY	1 CCTATCCTGTTTGTTAAGCCGGCGC 27 Db 7472 CCTATCCTGTTTGTTAAGCCGGCGC 7498			
RESULT 35				
LOCUS	AR035513 10851 bp DNA linear PAT 29-SEP-1999			
DEFINITION	Sequence 16 from patent US 5871910.			
ACCESSION	AR035513			
VERSION	AR035513.1 GI:5952181			
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 10851)			
TITLE	Arthur,M., Dikta-Malen,S., Molinas,C. and Courvailln,P.			
JOURNAL	Probes for the detection of nucleoside sequences implicated in the			
FEATURES	expression of resistance to glycopeptides, in particular in			
source	gram-positive bacteria			
	Patent: US 5871910-A 16 16-FEB-1999;			
	Location/Qualifiers			
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ORIGIN	Query Match 100.0%; Score 27; DB 6; Length 10851; Best Local Similarity 100.0%; Pred. No. 0.37; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 CCTATCCTGTTTGTTAAGCCGGCGC 27 			

Db 7472 CCTATCCTGTTTGTAAAGCCGCGC 7498

RESULT 36
LOCUS BD181854 10851 bp DNA linear PAT 15-MAY-2003
DEFINITION Polypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nucleotide sequence coding for these polypeptides and use for diagnosis.
ACCESSION BD181854
VERSION BD181854.1 GI:30792772
KEYWORDS JP 2002320494-A/10.
SOURCE unidentified
ORGANISM unidentified

REFERENCE
AUTHORS 1 (bases 1 to 10851)
TITLE Arthur M., Dukcamalen S., Molinas C. and Courvalin P.
JOURNAL Polypeptides implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria, nucleotide sequence coding for these polypeptides and use for diagnosis
PATENT: JP 2002320494-A 10 05-NOV-2002;
INSTITUT PASTEUR

COMMENT
OS Bacteria
PN JP 2002320494-A/10
PD 05-NOV-2002
PF 21-FEB-2002 JP 2002045484
PR 31-OCT-1990 FR 90/13579
PI MICHEL ARTHUR, SYLVIE DUKTA-MALEN, CATHERINE MOLINAS, PATRICE COURVALIN

PC C12N15/09, C07K14/315, C07K16/12, C12N1/15, C12N1/19, C12N1/21, PC C12N5/10,
PC C12Q1/04, C12Q1/68, G01N33/53, G01N33/566, G01N33/569//C12P21/08,
PC C12Q1/04, C12R1/01, C12Q1/68, C12R1/01, C12N15/00, C12N5/00 CC
Polypeptides implicated in the expression of resistance to CC
glycopeptides, in gram-positive bacteria, nucleotide sequence
CC in particular in gram-positive bacteria, nucleotide sequence
CC coding for
CC these polypeptides and use for diagnosis
FH Key Location/Qualifiers
FT source 1..10851
FT /organism="Bacteria",
Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 10851;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTAAAGCCGCGC 27
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7472 CCTATCCTGTTTGTAAAGCCGCGC 7498

Db 7472 CCTATCCTGTTTGTAAAGCCGCGC 7498

RESULT 37
LOCUS AX085648 10851 bp DNA linear PAT 09-MAR-2001
DEFINITION Sequence 1 from Patent WO0112803.
ACCESSION AX085648
VERSION AX085648.1 GI:13275634
KEYWORDS
SOURCE Enterococcus faecium
ORGANISM Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE
AUTHORS 1
TITLE Inouye, R.T., Torres-Viera, C., Moellerling, R., Gold, H. and Eliopoulos, G.M.
Methods and compositions for restoring antibiotic susceptibility in glycopeptide-resistant Enterococcus

JOURNAL Patent: WO 0112803-A 1 22-FEB-2001;
Beth Israel Deaconess Medical Center, Inc. (US)

FEATURES
source
Location/Qualifiers
1..10851
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/db_xref="taxon:1352"

ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 10851;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTAAAGCCGCGC 27
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7472 CCTATCCTGTTTGTAAAGCCGCGC 7498

Db 7472 CCTATCCTGTTTGTAAAGCCGCGC 7498

RESULT 38
LOCUS AF516335 17510 bp DNA linear BCT 28-AUG-2002
DEFINITION Enterococcus faecium plasmid pUW786 multiple antibiotic resistance gene cluster, complete sequence.
ACCESSION AF516335
VERSION AF516335.1 GI:21886737
KEYWORDS
SOURCE
ORGANISM Enterococcus faecium
Enterococcus faecium
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae;
Enterococcus.

REFERENCE
AUTHORS 1 (bases 1 to 17510)
TITLE Werner, G., Klare, I. and Witte, W.
JOURNAL Multi-resistance gene cluster on a plasmid in a clinical isolate of Enterococcus faecium
Unpublished
REFERENCE 2 (bases 1 to 17510)
AUTHORS Werner, G.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-2002) Wernigerode Branch, Robert Koch Institute, Buxteh.
37, Wernigerode 38855, Germany

FEATURES
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Location/Qualifiers
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VIERLRFGCKVLAYSRSRSIEVNVYVPELLONSDIVTLHVLPLNTDTHYIISHQIO
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sequence similarity; putative"
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similarity; putative"
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LAIVFPELPLFTLRACVFPIMLLNLINGPVPVIGLLFGTLTGTLTIPSTKKN
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by sequence similarity; putative"

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Db	34792	CCNATCCTGTTTGTGTTAAAGCCGCGC 34818
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LOCUS	BCY15704	
DEFINITION	<i>Bacillus circulans</i> vana gene.	
ACCESSION	Y15704	
VERSION	Y15704.1 GI:6448487	
KEYWORDS	vana gene.	
SOURCE	<i>Bacillus circulans</i>	
ORGANISM	<i>Bacillus circulans</i>	
REFERENCE	<i>Bacteria</i> ; Firmicutes; Bacillales; Bacillaceae; <i>Bacillus</i> .	
AUTHORS	1	
TITLE	Ligozzi, M., Lo Cascio, G. and Fontana, R.	
JOURNAL	vana gene cluster in a vancomycin-resistant clinical isolate of	
REFERENCE	<i>Bacillus circulans</i>	
AUTHORS	<i>Antimicrob. Agents Chemother.</i> 42 (8), 2055-2059 (1998)	
TITLE	9687406	
JOURNAL	2 (Bases 1 to 1054)	
REFERENCE	Ligozzi, M.	
AUTHORS	Direct Submission	
TITLE	Submitted (24-NOV-1997) M. Ligozzi, Universita di Verona, Istituto	
JOURNAL	di Microbiologia, Strada 1e Grazie 8, 37100 Verona, ITALY	
FEATURES	Location/Qualifiers	
SOURCE.	1..1054	
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ORIGIN
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Search completed: April 9, 2006, 07:14:32
Job time : 1052.14 secs

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95	17.6	65.2	39982	8	AAD48290	Aad48290 Human enz
96	17.6	65.2	66685	4	AAS07380	Aas07380 Human gen
97	17.6	65.2	66686	6	ABS73148	AbS73148 Human CLA
98	17.4	64.4	318	10	ACF68191	AcF68191 Photorhab
99	17.4	64.4	486	4	AAH34587	Aah34587 Human col
100	17.4	64.4	747	3	AAZ54529	Aaz54529 Neisseria
101	17.4	64.4	1053	12	AD062241	Ad062241 Transcrip
102	17.4	64.4	1053	11	ABD12733	Abd12733 Pseudomon
103	17.4	64.4	1260	13	ADXC0608	Adxc0608 Plant ful
104	17.4	64.4	1262	12	AD063288	Ad063288 Transcrip
105	17.4	64.4	1310	12	AD062242	Ad062242 Transcrip
106	17.4	64.4	1353	13	ADX53082	Adx53082 Plant ful
107	17.4	64.4	1512	11	ABD12707	Abd12707 Pseudomon
108	17.4	64.4	1865	12	AD062245	Ad062245 Transcrip
109	17.4	64.4	2334	11	ABD12689	Abd12689 Pseudomon
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112	17.4	64.4	23070	9	ADA02507	Ada02507 Mouse Wnt
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114	17.4	64.4	23070	10	AD895755	Ad895755 Mouse Wnt
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120	17.4	64.4	256525	11	ACM44148	AcM44148 Mouse gen

ALIGNMENTS

RESULT 1

ADY59929 standard; DNA; 27 BP.

ID ADY59929

AC ADY59929;

DT 02-JUN-2005 (first entry)

DE Enterococcus faecium vana probe SEQ ID NO:3.

XX DNA detection; antibiotic-resistance; vancomycin; vana; probe; ss.

XX Enterococcus faecium.

XX Synthetic.

XX US2005058985-A1.

XX 17-MAR-2005.

XX 12-SEP-2003; 2003US-00661094.

XX 12-SEP-2003; 2003US-00661094.

XX (DODG/) DODGSON K J.

XX Dodgson KJ;

XX WPI; 2005-222218/23.

XX Detecting vana and/or vana nucleic acid molecules in a sample, useful for

XX e.g. identifying vancomycin-resistant enterococcus, comprises using vana-

XX and/or vana-specific oligonucleotide probes or primers.

XX Claim 34; SEQ ID NO 3; 33pp; English.

XX The invention relates to a method for detecting vancomycin resistance

XX gene vana and/or vana nucleic acid molecules in a sample comprising

XX contacting the sample with a vana- and/or vana-specific oligonucleotide

XX probe or primer, and detecting or determining the presence or amount of

XX hybrid formation or amplified nucleic acid. Also described: (1) an

CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 898-917 of the vana gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 425-446 of the vana gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vana or vana DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vana gene and/or
CC vana gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vana and/or vana genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents a
CC probe for Enterococcus faecium vana, which is used in an example from the
CC present invention.

SQ Sequence 27 BP; 3 A; 8 C; 6 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 14; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.018; Mismatches 0; Gaps 0;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCTGTTTGTGTTAAGCCGCGCC 27

Db 1 CCTATCTGTTTGTGTTAAGCCGCGCC 27

RESULT 2

AAH02300 standard; DNA; 1032 BP.

ID AAH02300

AC AAH02300;

DT 24-JUL-2001 (first entry)

DE Enterococcus faecium nucleotide sequence SEQ ID NO:2293.

XX Species specific; genus specific; family specific; probe; detection;

XX identification; algal; archaeal; bacterial; fungal; parasitic;

XX microorganism; diagnosis; translation elongation factor Tu; toxin;

XX translation elongation factor G; RecA recombinase; resistance;

XX catalytic subunit of proton-translocating ATPase; antimicrobial;

XX primer; ds.

XX Enterococcus faecium.

XX WO200123604-A2.

XX 05-APR-2001.

XX 28-SEP-2000; 2000MO-CA001150.

XX 28-SEP-1999; 99CA-02283458.

XX 19-MAY-2000; 2000CA-02307010.

XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;

XX Picard FJ, Roy PH;

XX WPI; 2001-245006/25.

XX Nucleic acid sequences are used to generate universal probes and primers

XX which can be used to identify and detect the presence of algal, archaeal,

XX bacterial, fungal and parasitic species in a test sample.

XX Disclosure; Page 1578; 1580pp; English.

XX The present invention describes a method for generating a repository of

XX nucleic acids of tuf, fuv, atpD and/or recA genes from which probes

XX and/or primers are derived. The method comprises amplifying the nucleic

CC acids of determined algal, archaeal, bacterial, fungal and parasiticol
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasiticol species, genus, family and group. A nucleic acid (1) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexa nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (1) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Bactherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Naissaria
CC gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention

CC Sequence 1032 BP; 303 A; 197 C; 264 G; 268 T; 0 U; 0 Other;

CC Query Match 100.0%; Score 27; DB 4; Length 1032;

CC Best Local Similarity 100.0%; Pred. No. 0.03;

CC Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Db 1 CCTATCCTGTTTGTAAAGCGGCGC 27
CC 494 CCTATCCTGTTTGTAAAGCGGCGC 520

RESULT 3

CC ID AAF76039 standard; DNA; 1032 BP.

CC AC AAF76039;

CC XX 22-MAY-2001 (first entry)

CC DE Enterococcus faecium vanA gene, SEQ ID NO:21.

CC XX Vancomycin resistance reduction; antisense expression inhibition;

CC KM competitive inducer sequestration; vanH promoter; vanH gene product;

CC KM Enterococcus; Staphylococcus; Streptococcus; Gram-positive bacterium;

CC KM antibiotic susceptibility; ex vivo eradication; in vivo eradication;

CC KM glycopeptide resistance; VanA gene cluster; ds.

CC XX Enterococcus faecium.

CC XX WO200112803-A2.

CC XX 22-FEB-2001.

CC XX 11-AUG-2000; 2000WO-US022086.

CC XX 17-AUG-1999; 99US-0149313P.

CC XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

CC XX Inouye RT, Torres-Viera C, Moellering R, Gold H, Eliopoulos GM;

CC XX WPI, 2001-211216/21.

CC XX Reducing vancomycin-resistance in vancomycin-resistant organism by

CC XX introducing a antisense vancomycin-resistance molecule to inhibit

CC XX vancomycin-resistance gene expression, or by enhancing vanH promoter

CC XX expression.

CC XX Example; Page 52; 59pp; English.

CC The invention relates to methods of reducing vancomycin resistance in a
CC vancomycin-resistant organism. One method involves introducing a
CC vancomycin resistance gene antisense nucleic acid into the organism;
CC antisense oligonucleotides complementary to AAF76023-AAF76031 are
CC particularly preferred for this purpose. The second method involves
CC providing additional vanH promoter sequences which are not operatively
CC coupled to a vancomycin resistance gene, so that the phosphorylated vanH
CC gene product (which induces vanH promoter activity) is competitively
CC sequestered. Both methods are able to restore antibiotic susceptibility
CC in glycopeptide resistant enterococci. The methods of the invention are
CC useful for reducing vancomycin resistance in a vancomycin resistant
CC organism, particularly Enterococcus faecium and Enterococcus faecalis,
CC but also in other Gram-positive bacteria such as Staphylococcus sp. and
CC Streptococcus sp., to which Enterococcus faecium and Enterococcus
CC faecalis have the potential to transfer resistance determinants. The
CC antisense molecules are useful in the treatment of infection and
CC colonisation by vancomycin resistant enterococci and other clinically
CC significant pathogens, and may be used for the ex vivo eradication of
CC vancomycin-resistant enterococci from frequently colonised settings, such
CC as intensive care units, haemodialysis units, and chronic care facilities
CC ; for the in vivo clearance of vancomycin-resistant enterococci from
CC colonised gastrointestinal or genitourinary tracts of animals, including
CC humans; and in primary or adjuvant therapy for vancomycin-resistant
CC enterococcal infections. The gene based strategy targets key vancomycin
CC resistance determinants and results in restoration of vancomycin
CC susceptibility in previously glycopeptide-resistant enterococci.
CC Sequences AAF67036-AAF67042 represent genes of the Enterococcus faecium
CC VanA gene cluster

CC Sequence 1032 BP; 303 A; 197 C; 264 G; 268 T; 0 U; 0 Other;

CC Query Match 100.0%; Score 27; DB 4; Length 1032;

CC Best Local Similarity 100.0%; Pred. No. 0.03;

CC Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Db 1 CCTATCCTGTTTGTAAAGCGGCGC 27
CC 494 CCTATCCTGTTTGTAAAGCGGCGC 520

RESULT 4

CC ID AAH01064 standard; DNA; 1218 BP.

CC AC AAH01064;

CC XX 24-JUL-2001 (first entry)

CC DE Enterococcus gallinarum nucleotide sequence SEQ ID NO:1055.

CC XX Species specific; genus specific; family specific; probe; detection;

CC KM identification; algal; archaeal; bacterial; fungal; parasiticol;

CC KM microorganism; diagnosis; translation elongation factor Tu; toxin;

CC KM translation elongation factor G; RecA recombinase; resistance;

CC KM catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;

CC KM primer; ds.

CC XX Enterococcus gallinarum.

CC XX WO200123604-A2.

CC XX 05-APR-2001.

CC XX 28-SEP-2000; 2000WO-CA001150.

CC XX 28-SEP-1999; 99CA-02283458.

CC XX 19-MAY-2000; 2000CA-02307010.

CC XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

CC XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;

CC XX Picard FJ, Roy PH;

DR WPI; 2001-245006/25.

XX Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitological species in a test sample.

PS Claim 27; Page 1001-1002; 1580pp; English.

XX The present invention describes a method for generating a repertoire of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitological
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitological species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexa nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Baccharichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention

XX Sequence 1218 BP; 364 A; 226 C; 311 G; 317 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 27; DB 4; Length 1218;

XX Best Local Similarity 100.0%; Pred. No. 0.031;

XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTAAAGCCGCGC 27

DB 568 CCTATCCTGTTTGTAAAGCCGCGC 594

RESULT 5

AAH01063 standard; DNA; 1232 BP.

XX AAH01063;

XX 24-JUL-2001 (first entry)

XX Enterococcus faecalis nucleotide sequence SEQ ID NO:1054.

XX Species specific; genus specific; family specific; probe; detection;
XX identification; algal; archaeal; bacterial; fungal; parasitological;
XX microorganism; diagnosis; translation elongation factor Tu; toxin;
XX translation elongation factor G; RecA recombinase; resistance;
XX catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
XX primer; ds.

XX Enterococcus faecalis.

XX WO200123604-A2.

XX 05-APR-2001.

XX 28-SEP-2000; 2000WO-CA001150.

XX 28-SEP-1999; 99CA-02283458.

XX 19-MAY-2000; 2000CA-02307010.

PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;

PI Picard FU, Roy PH;

XX WPI; 2001-245006/25.

XX Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitological species in a test sample.

PS Claim 27; Page 1001; 1580pp; English.

XX The present invention describes a method for generating a repertoire of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitological
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitological species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexa nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Baccharichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention

XX Sequence 1232 BP; 367 A; 228 C; 313 G; 323 T; 0 U; 1 Other;

XX Query Match 100.0%; Score 27; DB 4; Length 1232;

XX Best Local Similarity 100.0%; Pred. No. 0.031;

XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTAAAGCCGCGC 27

DB 578 CCTATCCTGTTTGTAAAGCCGCGC 604

RESULT 6

AAH01061 standard; DNA; 1237 BP.

XX AAH01061;

XX 24-JUL-2001 (first entry)

XX Enterococcus faecium nucleotide sequence SEQ ID NO:1052.

XX Species specific; genus specific; family specific; probe; detection;
XX identification; algal; archaeal; bacterial; fungal; parasitological;
XX microorganism; diagnosis; translation elongation factor Tu; toxin;
XX translation elongation factor G; RecA recombinase; resistance;
XX catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
XX primer; ds.

XX Enterococcus faecium.

XX WO200123604-A2.

XX 05-APR-2001.

PF 28-SEP-2000; 2000MO-CA001150.
XX
XX 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX WPI; 2001-245006/25.
XX
XX Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitological species in a test sample.
XX
XX Claim 27; Page 999; 1580pp; English.
XX
XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitological
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection of an algal, archaeal, bacterial, fungal and
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitological species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection of
CC any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexa nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
CC
CC Sequence 1237 BP; 366 A; 235 C; 314 G; 322 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 27; DB 4; Length 1237;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTATCGTGTGTTGTTAGCGCGC 27
DB 590 CCTATCGTGTGTTGTTAGCGCGC 616
RESULT 7
AAH01058
ID AAH01058 standard; DNA; 1241 BP.
XX
XX AAH01058;
XX
XX 24-JUL-2001 (first entry)
DE Enterococcus faecium nucleotide sequence SEQ ID NO:1049.
XX
XX Species specific; genus specific; family specific; probe; detection;
XX identification; algal; archaeal; bacterial; fungal; parasitological;
XX microorganism; diagnosis; translation elongation factor Tu; toxin;
XX translation elongation factor G; RecA recombinase; resistance;
XX catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
XX primer; ds.
XX
XX Enterococcus faecium.
OS

XX
XX W0200123604-A2.
FN
XX
XX 05-APR-2001.
PD
XX
XX 28-SEP-2000; 2000MO-CA001150.
PF
XX
XX 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX WPI; 2001-245006/25.
XX
XX Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitological species in a test sample.
XX
XX Claim 27; Page 997; 1580pp; English.
XX
XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitological
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection of an algal, archaeal, bacterial, fungal and
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitological species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection of
CC any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexa nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
CC
CC Sequence 1241 BP; 371 A; 228 C; 317 G; 325 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 27; DB 4; Length 1241;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTATCGTGTGTTGTTAGCGCGC 27
DB 561 CCTATCGTGTGTTGTTAGCGCGC 587
RESULT 8
AAH01059
ID AAH01059 standard; DNA; 1249 BP.
XX
XX AAH01059;
XX
XX 24-JUL-2001 (first entry)
DE Enterococcus gallinarum nucleotide sequence SEQ ID NO:1050.
XX
XX Species specific; genus specific; family specific; probe; detection;
XX identification; algal; archaeal; bacterial; fungal; parasitological;
XX microorganism; diagnosis; translation elongation factor Tu; toxin;
XX

KW translation elongation factor G; RecA recombinase; resistance;
KM catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
XX primer; de.
OS Enterococcus gallinarum.
PN WO200123604-A2.
XX 05-APR-2001.
PD 28-SEP-2000; 2000WO-CA001150.
XX 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX WPI; 2001-245006/25.
XX
XX Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
XX Claim 27; Page 998; 1580pp; English.
XX
XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and for identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Baccharichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 1249 BP; 373 A; 235 C; 316 G; 325 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 27; DB 4; Length 1249;
XX Best Local Similarity 100.0%; Pred. No. 0.031;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CCGATCTGTTTGTGTTAAGCCGCGC 27
Db 590 CCGATCTGTTTGTGTTAAGCCGCGC 616
XX
XX
XX RESULT 9
XX AAH01062
XX ID AAH01062 standard; DNA; 1263 BP.
XX
XX AAH01062;
XX
XX 24-JUL-2001 (first entry)
XX

DE Enterococcus faecium nucleotide sequence SEQ ID NO:1053.
XX
XX Species specific; genus specific; family specific; probe; detection;
KM identification; algal; archaeal; bacterial; fungal; parasitical;
KM microorganisms; diagnosis; translation elongation factor Tu; toxin;
KM translation elongation factor G; RecA recombinase; resistance;
KM catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
XX primer; de.
OS Enterococcus faecium.
PN WO200123604-A2.
XX 05-APR-2001.
PD 28-SEP-2000; 2000WO-CA001150.
XX 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX WPI; 2001-245006/25.
XX
XX Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitical species in a test sample.
XX
XX Claim 27; Page 1000; 1580pp; English.
XX
XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and for identification of an algal, archaeal, bacterial, fungal and
CC parasitical species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Baccharichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
SQ Sequence 1263 BP; 378 A; 234 C; 321 G; 330 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 27; DB 4; Length 1263;
XX Best Local Similarity 100.0%; Pred. No. 0.031;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CCGATCTGTTTGTGTTAAGCCGCGC 27
Db 582 CCGATCTGTTTGTGTTAAGCCGCGC 608
XX
XX
XX RESULT 10
XX AAH01065
XX ID AAH01065 standard; DNA; 1265 BP.
XX

XX AAH01065;
AC 24-JUL-2001 (first entry)
DT
XX Enterococcus faecium nucleotide sequence SEQ ID NO:1056.
DE
XX Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitica;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
OS Enterococcus faecium.
PN WO200123604-A2.
XX
XX 05-APR-2001.
PD
XX 28-SEP-2000; 2000MO-CA001150.
PF
XX 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX WPI; 2001-24506/25.
XX
XX Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitica species in a test sample.
XX
XX Claim 27; Page 1002; 1580pp; English.
XX
XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitica
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitica species, genus, family and group. A nucleic acid (1) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexa nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (1) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
XX Sequence 1265 BP; 379 A; 237 C; 320 G; 329 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 27; DB 4; Length 1265;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX RESULT 11
XX AAH01066
ID AAH01066 standard; DNA; 1269 BP.
XX
XX AAH01066;
AC 24-JUL-2001 (first entry)
DT
XX Enterococcus faecium nucleotide sequence SEQ ID NO:1057.
DE
XX Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitica;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.
OS Enterococcus faecium.
PN WO200123604-A2.
XX
XX 05-APR-2001.
PD
XX 28-SEP-2000; 2000MO-CA001150.
PF
XX 28-SEP-1999; 99CA-02283458.
PR 19-MAY-2000; 2000CA-02307010.
XX
XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX WPI; 2001-24506/25.
XX
XX Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitica species in a test sample.
XX
XX Claim 27; Page 1003; 1580pp; English.
XX
XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitica
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitica species, genus, family and group. A nucleic acid (1) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexa nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (1) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH00010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention
XX
XX Sequence 1269 BP; 380 A; 238 C; 321 G; 330 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 27; DB 4; Length 1269;
Best Local Similarity 100.0%; Pred. No. 0.031;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCTATCCTGTTTGTAAAGCCGCGC 27
Db 590 CCTATCCTGTTTGTAAAGCCGCGC 616

RESULT 12

AAH01060
ID AAH01060 standard; DNA; 1272 BP.

AC AAH01060;

DT 24-JUL-2001 (first entry)

DE Enterococcus faecium nucleotide sequence SEQ ID NO:1051.

XX Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitica;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.

OS Enterococcus faecium.

PN WO200123604-A2.

PD 05-APR-2001.

PF 28-SEP-2000; 2000MO-CA001150.

PR 28-SEP-1999; 99CA-02283458.

PR 19-MAY-2000; 2000CA-02307010.

PA (INFR-) INFECTIO DIAGNOSTIC (IDI) INC.

PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;

PI Picard FJ, Roy PH;

DR WPI; 2001-245006/25.

PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitica species in a test sample.

PS Claim 27; Page 998-999; 1580pp; English.

XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitica
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitica species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
CC gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
CC results than substrate specificity tests as results can be determined in
CC an hour and improved accuracy is also achieved. AAH0010 to AAH002304
CC represent nucleotide sequences and primers/probes which are given in the
CC exemplification of the present invention

XX SQ Sequence 1272 BP; 379 A; 232 C; 325 G; 336 T; 0 U; 0 Other;
Query Match 100.0%; Score 27; DB 4; Length 1272;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13

AAH01148
ID AAH01148 standard; DNA; 1768 BP.

AC AAH01148;

DT 24-JUL-2001 (first entry)

DE Enterococcus faecium nucleotide sequence SEQ ID NO:1139.

XX Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitica;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KW primer; ds.

OS Enterococcus faecium.

PN WO200123604-A2.

PD 05-APR-2001.

PF 28-SEP-2000; 2000MO-CA001150.

PR 28-SEP-1999; 99CA-02283458.

PR 19-MAY-2000; 2000CA-02307010.

PA (INFR-) INFECTIO DIAGNOSTIC (IDI) INC.

PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;

PI Picard FJ, Roy PH;

DR WPI; 2001-245006/25.

PT Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitica species in a test sample.

PS Disclosure; Page 1033-1034; 1580pp; English.

XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitica
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal and
CC parasitica species, genus, family and group. A nucleic acid (I) obtained
CC using the method of the invention can be used for the universal detection
CC of any bacterium, fungus or parasite in a sample and for the detection of
CC at least one antimicrobial agent resistance gene or at least one toxin
CC gene. hexA nucleic acids are used for the specific and ubiquitous
CC detection and for identification of Streptococcus pneumoniae. (I) can be
CC used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria

gonorrhoeae and *Staphylococcus* sp. . Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AH00010 to AH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention

Sequence 1768 BP; 537 A; 336 C; 437 G; 458 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 1768;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCTATCCTGTTTGTGTTAAGCGGCGC 27
Db 870 CCTATCCTGTTTGTGTTAAGCGGCGC 896

RESULT 14

ADO47257 ADO47257 standard; DNA; 1768 BP.

AC ADO47257;

DT 15-JUN-2004 (first entry)

DE E. faecium vancomycin resistance gene, vanA.

KW Vancomycin resistant enterococcus; vancomycin resistance gene; vanA;

KM gene; ds; hospital acquired infection; VRE;

OS fluorescence resonance energy transfer; FRET.

XX Enterococcus faecium.

XX US2004058336-A1.

XX 25-MAR-2004.

XX 25-SEP-2002; 2002US-00254260.

XX 25-SEP-2002; 2002US-00254260.

PA (COCK)/ COCKERILL F R.

PA (SLOAN)/ SLOAN L M.

PI Cockerill FR, Sloan LM;

DR WPI; 2004-268785/25.

PT Detecting presence or absence of vancomycin-resistant enterococci in biological sample from individual comprises using real time polymerase chain reaction.

PS Disclosure; SEQ ID NO 10; 23pp; English.

The invention relates to detecting the presence or absence of vancomycin-resistant enterococci (VRE) in a sample, comprising performing a cycling step by amplifying a sample with pair of vanA or vanB primers and hybridising the sample with a pair of vanA or vanB probes, labelled with donor and acceptor fluorescent groups, respectively, detecting fluorescence resonance energy transfer (FRET), where the presence of FRET indicates presence of VRE. Also included is an article of manufacture, comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes and a donor fluorescent group and a corresponding fluorescent group. The method is useful for detecting the presence or absence of vancomycin-resistant enterococci in a biological sample, e.g. stool samples, anal or perirectal swabs, blood and body fluids from an individual. The method replaces standard culture methods and reduces the cost. The method provides rapid vancomycin resistant enterococcus real time PCR assay which is useful for beginning the antimicrobial therapy immediately to treat hospital acquired infection. The present sequence is an enterococcal vanA, vancomycin resistance gene.

Sequence 1768 BP; 537 A; 336 C; 437 G; 458 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 12; Length 1768;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCTATCCTGTTTGTGTTAAGCGGCGC 27
Db 870 CCTATCCTGTTTGTGTTAAGCGGCGC 896

RESULT 15

ADY59927 ADY59927 standard; DNA; 1768 BP.

AC ADY59927;

DT 02-JUN-2005 (first entry)

DE Enterococcus faecium vanA DNA sequence SEQ ID NO:1.

KW DNA detection; antibiotic-resistance; vancomycin; vanA; gene; ds.

OS Enterococcus faecium.

XX US2005058985-A1.

XX 17-MAR-2005.

XX 12-SEP-2003; 2003US-00661094.

XX 12-SEP-2003; 2003US-00661094.

PA (DODG)/ DODGSON K J.

PA Dodgson KJ;

DR WPI; 2005-222218/23.

PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for e.g. identifying vancomycin-resistant enterococcus, comprises using vanA- and/or vanB-specific oligonucleotide probes or primers.

PS Example 1; SEQ ID NO 1; 33pp; English.

The invention relates to a method for detecting vancomycin resistance gene vanA and/or vanB nucleic acid molecules in a sample comprising contacting the sample with a vanA- and/or vanB-specific oligonucleotide probe or primer, and detecting or determining the presence or amount of hybrid formation or amplified nucleic acid. Also described: (1) an oligonucleotide composition comprising a first oligonucleotide comprising sequences substantially corresponding to nucleotides 870-896, 851-868 or 898-917 of the vanA gene, or its complement or portion, or an oligonucleotide comprising sequences substantially corresponding to CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its complement or portion, where the oligonucleotide hybridises under stringent hybridization conditions to vanA or vanB DNA; and (2) a kit comprising one or more oligonucleotide(s) specific for a vanA gene and/or vanB gene in a test sample, comprising the oligonucleotide mentioned above. The method and kit are useful for detecting and/or amplifying genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying antibiotic resistance genes (e.g. vancomycin-resistant enterococcus). They may also be used in other industrial purposes, such as for quality control of food, water, pharmaceutical products or other products requiring microbiological control. The present sequence represents an Enterococcus faecium vanA nucleotide sequence from the present invention.

Sequence 1768 BP; 537 A; 336 C; 437 G; 458 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 14; Length 1768;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCTATCCTGTTTGTGTTAAGCGGCGC 27

Db 870 CCTATCCTGTTTGTGTTAAGCCGCGC 896

RESULT 16

AAT28569
ID AAT28569 standard; DNA; 2607 BP.

XX AAT28569;

DT 01-APR-1997 (first entry)

DE Bacterial antibiotic resistance gene, vanH, vanA and vanX, probe.

XX Detection; probe; amplification primer; bacterial pathogen; pneumonia;
XX *Escherichia coli*; *Klebsiella pneumoniae*; *Pseudomonas aeruginosa*;
XX *Streptococcus epidermidis*; *Enterococcus faecalis*; respiratory tract;
XX *Staphylococcus saprophyticus*; *Streptococcus pyogenes*; urinary tract;
XX *Haemophilus influenzae*; *Moraxella catarrhalis*; septicemia; meningitis;
XX infection; intra-abdominal infection; skin infection;
XX bacterial resistance; beta-lactam antibiotic; ds.

XX Synthetic.

PN MO9608582-A2.

PD 21-MAR-1996.

PF 12-SEP-1995; 95WO-CA000528.

PR 12-SEP-1994; 94US-00304732.

XX (BERG/) BERGERON M. G.
XX (OUEL/) OUELLETTE M.
XX (ROY/) ROY P. H.

PI Bergeron MG, Ouellette M, Roy PH;

DR WPI; 1996-179953/18.

PT Method for the detection of bacterial species using probes and primers -
PT allows detection and quantification of antibiotic resistant bacteria in
PT patients, the environment and food.

XX Claim 94; Page 145-147; 216pp; English.

XX The sequences given in AAT28560-76 represent fragments derived from
CC bacterial antibiotic resistance genes which were used as probes in the
CC method of the invention for the detection of bacterial species in a
CC sample. The method of the invention comprises using probes and/or
CC amplification primers which are specific, ubiquitous and sensitive for
CC determining the presence and/or amount of nucleic acids from selected
CC bacterial species in any sample, where the bacterial nucleic acid
CC comprises a selected target region hybridisable with the probes or
CC primers. The method comprises contacting the sample with the probes or
CC primers and detecting the presence and/or amount of hybridised primers or
CC amplification products as an indication of the presence and/or amount of
CC the bacterial species. This method may be used to detect commonly
CC encountered bacterial pathogens, e.g. *Escherichia coli*, *Klebsiella*
CC *pneumoniae*, *Pseudomonas aeruginosa*, *Streptococcus pyogenes*,
CC *Staphylococcus aureus*, *Staphylococcus epidermidis*,
CC *Enterococcus faecalis*, *Staphylococcus saprophyticus*, *Streptococcus*
CC *pyogenes*, *Haemophilus influenzae* and *Moraxella catarrhalis*. These
CC bacterial species are associated with approx. 90% of urinary tract
CC infections and with a high percentage of other severe infections,
CC including septicemia, meningitis, pneumonia, intra-abdominal infections,
CC skin infections and other severe respiratory tract infections. The method
CC may also be used to evaluate a bacterial resistance to beta-lactam
CC antibiotics

SQ Sequence 2607 BP; 768 A; 506 C; 652 G; 681 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 2; Length 2607;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTGTTAAGCCGCGC 27
DB 1455 CCTATCCTGTTTGTGTTAAGCCGCGC 1481

RESULT 17

ABA76994

ID ABA76994 standard; DNA; 2607 BP.

XX ABA76994;

DT 28-JAN-2002 (first entry)

DE Antibiotic resistance detection polynucleotide SEQ ID NO 170.

XX Detection; bacterial species; animal; food; environment;
XX antibiotic resistance; ds.

XX Unidentified.

PN NZS01596-A.

PD 29-JUN-2001.

PF 12-SEP-1995; 95NZ-00501596.

PR 12-SEP-1995; 95NZ-00501596.

PA (IDI-) IDI INFECTION DIAGNOSTIC INC.

PI Bergeron MG, Ouellette M, Roy PH;

DR WPI; 2001-615034/71.

PT Method for detecting target bacterial species in a sample, comprises
PT detecting the presence or amount of bacterial nucleic acid amplified by a
PT primer derived from bacterial DNA, specific for the target bacterial
PT species.

XX Claim 16; Page 160-162; 168pp; English.

XX The invention relates to detecting target bacterial species suspected to
CC be present in a sample, comprising contacting nucleic acids of target
CC bacterial species with an amplification primer pair derived from a
CC bacterial DNA fragment (ABA76825-ABA76861) specific for the target
CC bacterial species but ubiquitous for different strains, amplifying the
CC nucleic acid and detecting the presence or amount of an amplified
CC sequence as an indication of the presence or amount of the target
CC bacterial species. The invention includes primers and probes (ABA76862-
CC ABA76984) against the target bacterial species, especially *E. coli*,
CC *K. pneumoniae*, *P. aeruginosa*, *S. saprophyticus*, *S. pneumoniae*, *S. aureus*,
CC *M. catarrhalis* and/or group A *Streptococcus* producing exotoxin A gene spe
CC A, suspected to be present in a sample which is obtained from human
CC patients, animals, environment or food, and which consists of one or more
CC bacterial colonies. Oligonucleotide probes and primers complementary to
CC the bacterial genes encoding resistance to antibiotics such as bla(tem),
CC bla(rob), bla(shv), aacB, aacC1, aacC2, aacC3, aacA4, meca, vanA, vanH,
CC vanX, sacA, aacA-phd, vat, vga, mraA, sul and/or int (ABA76985-ABA77001)
CC are also useful to identify commonly encountered and clinically important
CC resistance genes. The invention provides a rapid method of bacterial
CC identification that can be achieved, which reduces the time currently
CC required for the identification of pathogens in the clinical laboratory

SQ Sequence 2607 BP; 768 A; 506 C; 652 G; 681 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 4; Length 2607;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTGAACCGCGGC 27
 DB 1455 CCTATCCTGTTTGTGAACCGCGGC 1481

RESULT 18
 ID AAH01150 standard; DNA; 3946 BP.

AAH01150;

24-JUL-2001 (first entry)

Enterococcus faecium nucleotide sequence SEQ ID NO:1141.

Species specific; genus specific; family specific; probe; detection;
 identification; algal; archaeal; bacterial; fungal; parasitica;
 microorganism; diagnosis; translation elongation factor Tu; toxin;
 translation elongation factor G; RecA recombinase; resistance;
 catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
 primer; ds.

Enterococcus faecium.

MO200123604-A2.

05-APR-2001.

28-SEP-2000; 2000WO-CA001150.

28-SEP-1999; 99CA-02283458.

19-MAY-2000; 2000CA-02307010.

(INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M,
 Picard FJ, Roy PH;

WPI; 2001-245006/25.

Nucleic acid sequences are used to generate universal probes and primers
 which can be used to identify and detect the presence of algal, archaeal,
 bacterial, fungal and parasitica species in a test sample.

Disclosure; Page 1035-1036; 1580pp; English.

The present invention describes a method for generating a repository of
 nucleic acids of tuf, fus, atpD and/or recA genes from which probes
 and/or primers are derived. The method comprises amplifying the nucleic
 acids of determined algal, archaeal, bacterial, fungal and parasitica
 species with a combination of defined primer pairs. The method can be
 used for producing probes and/or primers for detecting one or more
 related microorganisms e.g. algae, archaea, bacteria, fungi and
 parasites, for universal detection and for specific and ubiquitous
 detection and identification of an algal, archaeal, bacterial, fungal and
 parasitica species, genus, family and group. A nucleic acid (1) obtained
 using the method of the invention can be used for the universal detection
 of any bacterium, fungus or parasite in a sample and for the detection of
 at least one antimicrobial agent resistance gene or at least one toxin
 gene. hexa nucleic acids are used for the specific and ubiquitous
 detection and for identification of Streptococcus pneumoniae. (1) can be
 used to design a therapeutic agent which is effective against
 microorganisms. Microbial species or genus or family or phylum or group
 which can be detected include Abiotrophia adiacens, Bordetella sp.,
 Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
 Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
 gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
 results than substrate specificity tests as results can be determined in
 an hour and improved accuracy is also achieved. AAH00010 to AAH002304
 CC represent nucleotide sequences and primers/probes which are given in the
 CC exemplification of the present invention

Sequence 3946 BP; 1235 A; 706 C; 936 G; 1065 T; 0 U; 0 Other;

Query Match

100.0%; Score 27; DB 4; Length 3946;

Best Local Similarity 100.0%; Pred. No. 0.037;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTGAACCGCGGC 27
 DB 1455 CCTATCCTGTTTGTGAACCGCGGC 1481

RESULT 19
 ID AAQ25183 standard; DNA; 7227 BP.

AAQ25183;

24-OCT-2003 (revised)

25-MAR-2003 (revised)

20-NOV-1992 (first entry)

E.faecium antibiotic resistance genes and flanking sequences.

Glycopeptide antibiotic; vancomycin; telicoplanin; resistant;

D-Ala-D-Ala ligase; peptidoglycan precursor; transposon;

inverted repeats; vanR; vanS; vanH; vanA; vanX; se.

Enterococcus faecium; BM4147.

MO207942-A1.

14-MAY-1992.

29-OCT-1991; 91WO-FR000855.

31-OCT-1990; 90FR-00013579.

(INSP) INST PASTEUR.

Arthur M, Dutka-Malen S, Molinas C, Courvalin P;

WPI; 1992-183677/22.

P-PSDB; AAR24305, AAR24306, AAR24307.

Polypeptides involved in expression of glycopeptide antibiotic resistance

- useful in diagnosing presence of Gram-positive enterococcal strains

e.g. Enterococcus faecium and E. Gallinarum.

Disclosure; Fig 4; 163pp; French.

This sequence contains the genes vanH, vanA, vanX, vanR and vanS. The

proteins encoded by the latter two genes (i.e. proteins VanR and Vans)

have a regulatory function and control expression of the other three

("protective") proteins. See also AAQ25179-025182. (Updated on 25-MAR-

2003 to correct PI field.) (Updated on 25-MAR-2003 to correct PI field.)

(Updated on 24-OCT-2003 to standardise OS field)

Sequence 7227 BP; 2313 A; 1305 C; 1596 G; 2011 T; 0 U; 2 Other;

Query Match

100.0%; Score 27; DB 2; Length 7227;

Best Local Similarity 100.0%; Pred. No. 0.04;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTGAACCGCGGC 27
 DB 5018 CCTATCCTGTTTGTGAACCGCGGC 5044

RESULT 20

AAQ25178 standard; DNA; 10851 BP.

AAQ25178;

XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 20-NOV-1992 (first entry)
XX E. faecium antibiotic resistance genes and Tn sequences.
XX Glycopeptide antibiotic; vancomycin; telicoplanin; resistant;
KM D-Ala-D-Ala ligase; peptidoglycan precursor; transposon;
KM inverted repeats; ss.
XX Enterococcus faecium; BM4147.
XX Key location/Qualifiers
FH complement (1..3189)
FT CDS /tag= a
FT /product= "transposase"
FT /note= "coded by the (-) strand - see AAQ25179"
FT repeat_unit
FT 1..38
FT /tag= j
FT /rpt_type= INVERTED
FT 3187..33762
FT /tag= b
FT /product= "resolvase"
FT 3976..4671
FT CDS /tag= c
FT /product= "VanR"
FT /note= "VanR is a transcription activator"
FT 4649..5803
FT /tag= d
FT /product= "Vans"
FT /note= "Vans is a regulatory protein"
FT 6018..6986
FT /tag= e
FT /product= "VanH"
FT 6979..8010
FT CDS /tag= f
FT /product= "Vana"
FT 8016..8624
FT /tag= g
FT /product= "VanX"
FT 9052..9963
FT CDS /tag= h
FT /product= "Vany"
FT 10116..10601
FT /tag= i
FT /product= "Vanz"
FT repeat_unit
FT complement (10814..10851)
FT /tag= k
FT /rpt_type= INVERTED
XX W09207942-A1.
XX 14-MAY-1992.
XX 29-OCT-1991; 91WO-FR000855.
XX 31-OCT-1990; 90FR-00013579.
XX (INSP) INST PASTEUR.
XX Arthur M, Dukta-Malen S, Molinas C, Courvalin P;
XX WPI; 1992-183677/22.
XX P-PSDB; AAR24295, AAR24296, AAR24297, AAR24298, AAR24299,
XX AAR24300, AAR24301, AAR24302.
XX Polypeptides involved in expression of glycopeptide antibiotic resistance
PT - useful in diagnosing presence of Gram-positive enterococcal strains
PT e.g. Enterococcus faecium and E. Gallinarum.
XX Claim 9; Fig 8; 163pp; French.
XX

CC This is a transposon sequence. The transposon comprises the genes
CC necessary for expression of resistance to glycopeptides in Enterococcus
CC faecium. It also contains genes associated with resistance, e.g. involved
CC in regulation of expression of the resistance genes or in the amount of
CC polypeptides produced. See also AAQ25179-Q25183. (Updated on 25-MAR-2003
CC to correct PM field.) (Updated on 25-MAR-2003 to correct FI field.)
CC (Updated on 24-OCT-2003 to standardise OS field)
XX SQ Sequence 10851 BP; 3399 A; 1960 C; 2234 G; 3258 T; 0 U; 0 Other;
Query Match 100.0%; Score 27; DB 2; Length 10851;
Best Local Similarity 100.0%; Pred. No. 0.042; Indels 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCTATCCTGTTTGTAAAGCCGCGCC 27
Db 7472 CCTATCCTGTTTGTAAAGCCGCGCC 7498
RESULT 21
AAAF76019
ID AAFA76019 standard; DNA; 10851 BP.
AC AAFA76019;
XX 22-MAY-2001 (first entry)
DE E. faecium Vana vancomycin resistance gene cluster, SEQ ID NO:1.
XX Vancomycin resistance reduction; antisense expression inhibition;
XX competitive inducer sequestration; vanh promoter; vanr gene product;
XX Enterococcus; Staphylococcus; Streptococcus; Gram-positive bacterium;
XX antibiotic susceptibility; ex vivo eradication; in vivo eradication;
XX glycopeptide resistance; Vana gene cluster; de.
XX Enterococcus faecium.
OS W0200112803-A2.
XX W0200112803-A2.
XX 22-FEB-2001.
XX 11-AUG-2000; 2000MO-US022086.
XX 17-AUG-1999; 99US-0149313P.
XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX Inouye RT, Torres-Viera C, Moellering R, Gold H, Eliopoulos GM;
XX WPI; 2001-211216/21.
XX Reducing vancomycin-resistance in vancomycin-resistant organism by
PT introducing a antisense vancomycin-resistance molecule to inhibit
PT vancomycin-resistance gene expression, or by enhancing vanh promoter
PT expression.
XX Claim 24; Page 41-44; 59pp; English.
XX The invention relates to methods of reducing vancomycin resistance in a
CC vancomycin-resistant organism. One method involves introducing a
CC vancomycin resistance gene antisense nucleic acid into the organism;
CC antisense oligonucleotides complementary to AAFA76023-AAFA76031 are
CC particularly preferred for this purpose. The second method involves
CC providing additional vanh promoter sequences which are not operatively
CC coupled to a vancomycin resistance gene, so that the phosphorylated vanr
CC gene product (which induces vanh promoter activity) is competitively
CC sequestered. Both methods are able to restore antibiotic susceptibility
CC in glycopeptide resistant enterococci. The methods of the invention are
CC useful for reducing vancomycin resistance in a vancomycin resistant
CC organism, particularly Enterococcus faecium and Enterococcus faecalis,
CC but also in other Gram-positive bacteria such as Staphylococcus sp. and
CC Streptococcus sp., to which Enterococcus faecium and Enterococcus
CC faecalis have the potential to transfer resistance determinants. The

CC antisense molecules are useful in the treatment of infection and
CC colonization by vancomycin resistant enterococci and other clinically
CC significant pathogens, and may be used for the ex vivo eradication of
CC vancomycin-resistant enterococci from frequently colonized settings, such
CC as intensive care units, haemodialysis units, and chronic care facilities
CC ; for the in vivo clearance of vancomycin-resistant enterococci from
CC colonized gastrointestinal or genitourinary tracts of animals, including
CC humans; and in primary or adjuvant therapy for vancomycin-resistant
CC enterococcal infections. The gene based strategy targets key vancomycin
CC resistance determinants and results in restoration of vancomycin
CC susceptibility in previously glycopeptide-resistant enterococci. The
CC present sequence represents the Enterococcus faecium Vana gene cluster
SQ Sequence 10851 BP; 3392 A; 1962 C; 2237 G; 3260 T; 0 U; 0 Other;
Qy Query Match 100.0%; Score 27; DB 4; Length 10851;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 CCGATCCGTTTGTGTTAAGCCGCGC 27
7472 CCGATCCGTTTGTGTTAAGCCGCGC 7498
RESULT 22
ACA22997
ID ACA22997 standard; DNA; 1071 BP.
XX
AC ACA22997;
XX
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #4654.
XX
KM Antisense; de; prokaryotic essential gene; cell proliferation;
XX drug design; gene.
XX
OS Borrelia burgdorferi.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
XX 06-SEP-2001; 2001US-00948993.
XX 25-OCT-2001; 2001US-0342923P.
XX 08-FEB-2002; 2002US-00072851.
XX 06-MAR-2002; 2002US-0362699P.
XX
PA (ELITRA PHARM INC.
XX
PI Wang J, Zamudio C, Malone C, Haselbeck R, Ohlsen KI, Zvekind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR MPI: 2003-029926/02.
XX P-PSDB; ABU19127.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 10867; 1766bp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 1071 BP; 335 A; 127 C; 198 G; 411 T; 0 U; 0 Other;
Qy Query Match 77.0%; Score 20.8; DB 8; Length 1071;
Best Local Similarity 91.7%; Pred. No. 21;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 2 CCGATCCGTTTGTGTTAAGCCGCGC 25
498 CCGATCCGTTTGTGTTAAGCCGCGC 521
RESULT 23
AAX20248_07
Continuation (8 of 10) of AAX20248 from base 700001 (Borrelia burgdorferi polynucleotide
WP Sequence split into 10 fragments LOCUS AAX20248 Accession Aax20248
WP Fragment Name Begin End
WP AAX20248_00 1 110000
WP AAX20248_01 100001 210000
WP AAX20248_02 200001 310000
WP AAX20248_03 300001 410000
WP AAX20248_04 400001 510000
WP AAX20248_05 500001 610000
WP AAX20248_06 600001 710000
WP AAX20248_07 700001 810000
WP AAX20248_08 800001 910000
WP AAX20248_09 900001 910715
Qy Query Match 77.0%; Score 20.8; DB 2; Length 110000;
Best Local Similarity 91.7%; Pred. No. 41;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 2 CCGATCCGTTTGTGTTAAGCCGCGC 25
10177 CCGATCCGTTTGTGTTAAGCCGCGC 10200
RESULT 24
ADO47266/c
ID ADO47266 standard; DNA; 555 BP.
XX
AC ADO47266;
XX
DT 15-JUL-2004 (first entry)
XX
DE Enterococcus vancomycin resistance gene, vanB ENEVANB2A.
XX
CC Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
CC gene; de; hospital acquired infection; VRB;
CC fluorescence resonance energy transfer; FRET.
KW

XX OS Enterococcus sp.
XX PN US2004058336-A1.
XX PD 25-MAR-2004.
XX PF 25-SEP-2002; 2002US-00254260.
XX PR 25-SEP-2002; 2002US-00254260.
XX PA (COCK/) COCKERILL F R.
XX PA (SLOA/) SLOAN L M.
XX PI Cockerill FR, Sloan LM;
XX DR WPI; 2004-268785/25.
XX PT Detecting presence or absence of vancomycin-resistant enterococci in
XX PT biological sample from individual comprises using real time polymerase
XX PT chain reaction.
XX PS Disclosure; SEQ ID NO 20; 23bp; English.
XX CC The invention relates to detecting the presence or absence of vancomycin-
XX CC resistant enterococci (VRE) in a sample, comprising performing a cycling
XX CC step by amplifying a sample with pair of vanA or vanB primers and
XX CC hybridising the sample with a pair of vanA or vanB probes, labelled with
XX CC donor and acceptor fluorescent group, respectively, detecting
XX CC fluorescence resonance energy transfer (FRET), where the presence of FRET
XX CC indicates presence of VRE. Also included is an article of manufacture,
XX CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
XX CC and a donor fluorescent group and a corresponding fluorescent group. The
XX CC method is useful for detecting the presence or absence of vancomycin-
XX CC resistant enterococci in a biological sample, e.g. stool samples, anal or
XX CC perirectal swabs, blood and body fluids from an individual. The method
XX CC replaces standard culture methods and reduces the cost. The method
XX CC provides rapid vancomycin resistant enterococcus real time PCR assay
XX CC which is useful for beginning the antimicrobial therapy immediately to
XX CC treat hospital acquired infection. The present sequence is an
XX CC enterococcal vanB, vancomycin resistance gene.
XX SQ Sequence 555 BP; 132 A; 161 C; 115 G; 145 T; 0 U; 2 Other;
XX
XX Query Match 76.3%; Score 20.6; DB 12; Length 555;
XX Best Local Similarity 85.2%; Pred. No. 23;
XX Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 CCTATCCTGTTTGTGTAAGCCGGCGC 27
XX Db 391 CCTACCTGTCCTTGTGTAAGCCGGCAC 365
XX
XX RESULT 25
XX ADO47264/c
XX ID ADO47264 standard; DNA; 556 BP.
XX AC ADO47264;
XX DT 15-JUL-2004 (first entry)
XX DE Enterococcus vancomycin resistance gene, vanB ENEVANB.
XX KM Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
XX KM gene; ds; hospital acquired infection; VRE;
XX KM fluorescence resonance energy transfer; FRET.
XX OS Enterococcus sp.
XX PN US2004058336-A1.
XX PD 25-MAR-2004.

XX PF 25-SEP-2002; 2002US-00254260.
XX XX
XX PR 25-SEP-2002; 2002US-00254260.
XX XX
XX PA (COCK/) COCKERILL F R.
XX PA (SLOA/) SLOAN L M.
XX PI Cockerill FR, Sloan LM;
XX DR WPI; 2004-268785/25.
XX XX
XX PT Detecting presence or absence of vancomycin-resistant enterococci in
XX PT biological sample from individual comprises using real time polymerase
XX PT chain reaction.
XX PS Disclosure; SEQ ID NO 18; 23bp; English.
XX CC The invention relates to detecting the presence or absence of vancomycin-
XX CC resistant enterococci (VRE) in a sample, comprising performing a cycling
XX CC step by amplifying a sample with pair of vanA or vanB primers and
XX CC hybridising the sample with a pair of vanA or vanB probes, labelled with
XX CC donor and acceptor fluorescent group, respectively, detecting
XX CC fluorescence resonance energy transfer (FRET), where the presence of FRET
XX CC indicates presence of VRE. Also included is an article of manufacture,
XX CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
XX CC and a donor fluorescent group and a corresponding fluorescent group. The
XX CC method is useful for detecting the presence or absence of vancomycin-
XX CC resistant enterococci in a biological sample, e.g. stool samples, anal or
XX CC perirectal swabs, blood and body fluids from an individual. The method
XX CC replaces standard culture methods and reduces the cost. The method
XX CC provides rapid vancomycin resistant enterococcus real time PCR assay
XX CC which is useful for beginning the antimicrobial therapy immediately to
XX CC treat hospital acquired infection. The present sequence is an
XX CC enterococcal vanB, vancomycin resistance gene.
XX SQ Sequence 556 BP; 130 A; 154 C; 117 G; 155 T; 0 U; 0 Other;
XX
XX Query Match 76.3%; Score 20.6; DB 12; Length 556;
XX Best Local Similarity 85.2%; Pred. No. 23;
XX Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 CCTATCCTGTTTGTGTAAGCCGGCGC 27
XX Db 392 CCTACCTGTCCTTGTGTAAGCCGGCAC 366
XX
XX RESULT 26
XX ADO47262/c
XX ID ADO47262 standard; DNA; 556 BP.
XX AC ADO47262;
XX DT 15-JUL-2004 (first entry)
XX DE E. faecalis vancomycin resistance gene, vanB EFU94526.
XX KM Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
XX KM gene; ds; hospital acquired infection; VRE;
XX KM fluorescence resonance energy transfer; FRET.
XX OS Enterococcus faecalis.
XX PN US2004058336-A1.
XX PD 25-MAR-2004.
XX PF 25-SEP-2002; 2002US-00254260.
XX PR 25-SEP-2002; 2002US-00254260.
XX PA (COCK/) COCKERILL F R.
XX PA (SLOA/) SLOAN L M.

PI Cockerill FR, Sloan LM;
XX
XX WPI; 2004-268785/25.
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 15; 23pp; English.
XX
XX The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanb or vanb primers and
CC hybridising the sample with a pair of vanb or vanb probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanb or vanb primers, a pair of vanb or vanb probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanb, vancomycin resistance gene.
XX
SQ Sequence 556 BP; 133 A; 162 C; 116 G; 145 T; 0 U; 0 Other;
Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
Db 392 CCTACCTGTTTGTGTAAGCGGCGC 366
RESULT 27
ADO47263/C
ID ADO47263 standard; DNA; 556 BP.
XX
XX AC ADO47263;
XX
DT 15-JUL-2004 (first entry)
XX
XX E. faecalis vancomycin resistance gene, vanb EFU94527.
XX
XX Vancomycin resistant enterococcus; vancomycin resistance gene; vanb;
XX gene; ds; hospital acquired infection; VRE;
XX fluorescence resonance energy transfer; FRET.
XX
XX Enterococcus faecalis.
XX
XX US2004058336-A1.
XX
XX 25-MAR-2004.
XX
XX 25-SEP-2002; 2002US-00254260.
XX
XX 25-SEP-2002; 2002US-00254260.
XX
XX (COCK/) COCKERILL F R.
XX (SLOA/) SLOAN L M.
XX
XX Cockerill FR, Sloan LM;
XX
XX WPI; 2004-268785/25.
XX
XX Detecting presence or absence of vancomycin-resistant enterococci in
XX biological sample from individual comprises using real time polymerase
XX chain reaction.

XX
XX Disclosure; SEQ ID NO 17; 23pp; English.
XX
XX
XX The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanb or vanb primers and
CC hybridising the sample with a pair of vanb or vanb probes, labelled with
CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanb or vanb primers, a pair of vanb or vanb probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanb, vancomycin resistance gene.
XX
SQ Sequence 556 BP; 130 A; 154 C; 117 G; 155 T; 0 U; 0 Other;
Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 CCTATCCTGTTTGTGTAAGCGGCGC 27
Db 392 CCTACCTGTTTGTGTAAGCGGCGC 366
RESULT 28
ADO47261/C
ID ADO47261 standard; DNA; 556 BP.
XX
XX AC ADO47261;
XX
DT 15-JUL-2004 (first entry)
XX
XX E. faecalis vancomycin resistance gene, vanb EFU94529.
XX
XX Vancomycin resistant enterococcus; vancomycin resistance gene; vanb;
XX gene; ds; hospital acquired infection; VRE;
XX fluorescence resonance energy transfer; FRET.
XX
XX Enterococcus faecalis.
XX
XX US2004058336-A1.
XX
XX 25-MAR-2004.
XX
XX 25-SEP-2002; 2002US-00254260.
XX
XX 25-SEP-2002; 2002US-00254260.
XX
XX (COCK/) COCKERILL F R.
XX (SLOA/) SLOAN L M.
XX
XX Cockerill FR, Sloan LM;
XX
XX WPI; 2004-268785/25.
XX
XX Detecting presence or absence of vancomycin-resistant enterococci in
XX biological sample from individual comprises using real time polymerase
XX chain reaction.
XX
XX Disclosure; SEQ ID NO 14; 23pp; English.
XX
XX The invention relates to detecting the presence or absence of vancomycin-
CC resistant enterococci (VRE) in a sample, comprising performing a cycling
CC step by amplifying a sample with pair of vanb or vanb primers and
CC hybridising the sample with a pair of vanb or vanb probes, labelled with

CC donor and acceptor fluorescent group, respectively, detecting
CC fluorescence resonance energy transfer (FRET), where the presence of FRET
CC indicates presence of VRE. Also included is an article of manufacture,
CC comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
CC and a donor fluorescent group and a corresponding fluorescent group. The
CC method is useful for detecting the presence or absence of vancomycin-
CC resistant enterococci in a biological sample, e.g. stool samples, anal or
CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.

XX
SQ Sequence 556 BP; 134 A; 161 C; 116 G; 145 T; 0 U; 0 Other;
Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
Db 392 CCTACCTGCTTGTGTAAGCCGCGC 366

RESULT 29
ADO47265/c
ID ADO47265 standard; DNA; 556 BP.
XX
AC ADO47265;
XX
DT 15-JUL-2004 (first entry)
XX
DE E. faecalis vancomycin resistance gene, vanB EFU72704.
XX
XX Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
XX gene; ds; hospital acquired infection; VRE;
XX fluorescence resonance energy transfer; FRET.
XX
OS Enterococcus faecalis.
XX
PN US2004058336-A1.
XX
PD 25-MAR-2004.
XX
PF 25-SEP-2002; 2002US-00254260.
XX
PR 25-SEP-2002; 2002US-00254260.
XX
PA (COCK/) COCKERILL F R.
XX (SLOA/) SLOAN L M.
XX
PI Cockerill FR, Sloan LM;
XX
PS WPI; 2004-268785/25.
XX
DR
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
XX Disclosure; SEQ ID NO 19; 23bp; English.

XX The invention relates to detecting the presence or absence of vancomycin-
XX resistant enterococci (VRE) in a sample, comprising performing a cycling
XX step by amplifying a sample with pair of vanA or vanB primers and
XX hybridizing the sample with a pair of vanA or vanB probes, labelled with
XX donor and acceptor fluorescent group, respectively, detecting
XX fluorescence resonance energy transfer (FRET), where the presence of FRET
XX indicates presence of VRE. Also included is an article of manufacture,
XX comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
XX and a donor fluorescent group and a corresponding fluorescent group. The
XX method is useful for detecting the presence or absence of vancomycin-
XX resistant enterococci in a biological sample, e.g. stool samples, anal or
XX perirectal swabs, blood and body fluids from an individual. The method
XX replaces standard culture methods and reduces the cost. The method
XX provides rapid vancomycin resistant enterococcus real time PCR assay
XX which is useful for beginning the antimicrobial therapy immediately to
XX treat hospital acquired infection. The present sequence is an
XX enterococcal vanB, vancomycin resistance gene.

CC perirectal swabs, blood and body fluids from an individual. The method
CC replaces standard culture methods and reduces the cost. The method
CC provides rapid vancomycin resistant enterococcus real time PCR assay
CC which is useful for beginning the antimicrobial therapy immediately to
CC treat hospital acquired infection. The present sequence is an
CC enterococcal vanB, vancomycin resistance gene.

XX
SQ Sequence 556 BP; 134 A; 158 C; 117 G; 147 T; 0 U; 0 Other;
Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
Db 392 CCTACCTGCTTGTGTAAGCCGCGC 366

RESULT 30
ADO47260/c
ID ADO47260 standard; DNA; 556 BP.
XX
AC ADO47260;
XX
DT 15-JUL-2004 (first entry)
XX
DE E. faecalis vancomycin resistance gene, vanB EFU94528.
XX
XX Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
XX gene; ds; hospital acquired infection; VRE;
XX fluorescence resonance energy transfer; FRET.
XX
OS Enterococcus faecalis.
XX
PN US2004058336-A1.
XX
PD 25-MAR-2004.
XX
PF 25-SEP-2002; 2002US-00254260.
XX
PR 25-SEP-2002; 2002US-00254260.
XX
PA (COCK/) COCKERILL F R.
XX (SLOA/) SLOAN L M.
XX
PI Cockerill FR, Sloan LM;
XX
PS WPI; 2004-268785/25.
XX
DR
XX
PT Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
XX Disclosure; SEQ ID NO 13; 23bp; English.

XX The invention relates to detecting the presence or absence of vancomycin-
XX resistant enterococci (VRE) in a sample, comprising performing a cycling
XX step by amplifying a sample with pair of vanA or vanB primers and
XX hybridizing the sample with a pair of vanA or vanB probes, labelled with
XX donor and acceptor fluorescent group, respectively, detecting
XX fluorescence resonance energy transfer (FRET), where the presence of FRET
XX indicates presence of VRE. Also included is an article of manufacture,
XX comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
XX and a donor fluorescent group and a corresponding fluorescent group. The
XX method is useful for detecting the presence or absence of vancomycin-
XX resistant enterococci in a biological sample, e.g. stool samples, anal or
XX perirectal swabs, blood and body fluids from an individual. The method
XX replaces standard culture methods and reduces the cost. The method
XX provides rapid vancomycin resistant enterococcus real time PCR assay
XX which is useful for beginning the antimicrobial therapy immediately to
XX treat hospital acquired infection. The present sequence is an
XX enterococcal vanB, vancomycin resistance gene.

SQ Sequence 556 BP; 134 A; 161 C; 116 G; 145 T; 0 U; 0 Other;
Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
DB 392 CCTACCTGTCTTGTGAAGCCGGCAG 366
OY 1 CCTATCCTGTTTGTGAAGCCGGC 27
ID ADO47259 standard; DNA; 556 BP.
XX ADO47259;
AC ADO47259;
XX 15-JUN-2004 (first entry)
XX E. faecalis vancomycin resistance gene, vanB EFU94530.
DE
XX Vancomycin resistant enterococcus; vancomycin resistance gene; vanB;
KM gene; ds; hospital acquired infection; VRE;
KM fluorescence resonance energy transfer; FRET.
XX Enterococcus faecalis.
OS
XX US2004058336-A1.
XX 25-MAR-2004.
XX 25-SEP-2002; 2002US-00254260.
XX 25-SEP-2002; 2002US-00254260.
XX (COCK/) COCKERILL F R.
XX (SLOA/) SLOAN L M.
XX Cockerill FR, Sloan LM;
PI WPI; 2004-268785/25.
XX
XX Detecting presence or absence of vancomycin-resistant enterococci in
PT biological sample from individual comprises using real time polymerase
PT chain reaction.
XX
XX Disclosure; SEQ ID NO 16; 23pp; English.
PS
XX The invention relates to detecting the presence or absence of vancomycin-
XX resistant enterococci (VRE) in a sample, comprising performing a cycling
XX step by amplifying a sample with pair of vanA or vanB primers and
XX hybridizing the sample with a pair of vanA or vanB probes, labelled with
XX donor and acceptor fluorescent group, respectively, detecting
XX fluorescence resonance energy transfer (FRET), where the presence of FRET
XX indicates presence of VRE. Also included is an article of manufacture,
XX comprising a pair of vanA or vanB primers, a pair of vanA or vanB probes
XX and a donor fluorescent group and a corresponding fluorescent group. The
XX method is useful for detecting the presence or absence of vancomycin-
XX resistant enterococci in a biological sample, e.g. stool samples, anal or
XX perirectal swabs, blood and body fluids from an individual. The method
XX replaces standard culture methods and reduces the cost. The method
XX provides rapid vancomycin resistant enterococcus real time PCR assay
XX which is useful for beginning the antimicrobial therapy immediately to
XX treat hospital acquired infection. The present sequence is an
XX enterococcal vanB, vancomycin resistance gene.
XX
SQ Sequence 556 BP; 134 A; 161 C; 116 G; 145 T; 0 U; 0 Other;
Query Match 76.3%; Score 20.6; DB 12; Length 556;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 CCTATCCTGTTTGTGAAGCCGGC 27

DB 392 CCTACCTGTCTTGTGAAGCCGGCAG 366
RESULT 32
ID AA069230 standard; DNA; 589 BP.
XX AA069230;
AC AA069230;
XX 25-MAR-2003 (revised)
XX 23-FEB-1995 (first entry)
XX
XX Enterococcus faecalis vanB gene (internal, amplified fragment).
DE
XX Gram positive bacteria; inducible glycopeptide resistance; vancomycin;
KM teicoplanin; antibiotic; vanB gene; ds.
XX Enterococcus faecalis.
OS
XX Key Location/Qualifiers
FH misc_feature 2..589
FT /tag= a
FT /note= "amplified internal fragment of vanB gene"
XX
XX FR2699539-A1.
XX 24-JUN-1994.
XX 18-DEC-1992; 92FR-00015671.
XX 18-DEC-1992; 92FR-00015671.
XX 18-DEC-1992; 92FR-00015671.
XX (INSP) INST PASTEUR.
XX Arthur M, Dutka-Malen S, Evers S, Courvalin P;
PI WPI; 1994-227159/28.
XX P-PSDB; AAR57150.
XX
XX New protein vanB involved in bacterial resistance to glyco-peptide(s) -
PT esp vancomycin, and related nucleic acid, vectors, transformed cells and
PT antibodies, for in vitro detection of resistant strains.
XX
XX Claim 8; Page 28; 39pp; French.
PS
XX The protein encoded by the vanB gene is implicated in resistance of Gram-
XX positive bacteria to glycopeptides, particularly to vancomycin. This
XX resistance is inducible by Vancomycin but not by teicoplanin. Sequence
XX AA069230 is a claimed internal fragment of the vanB gene. (Updated on 25-
XX MAR-2003 to correct PN field.)
SQ Sequence 589 BP; 163 A; 124 C; 166 G; 136 T; 0 U; 0 Other;
Query Match 76.3%; Score 20.6; DB 2; Length 589;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 CCTATCCTGTTTGTGAAGCCGGC 27
DB 165 CCTACCTGTCTTGTGAAGCCGGCAG 191
RESULT 33
ID ADY59941 standard; DNA; 630 BP.
XX ADY59941;
AC ADY59941;
XX 02-JUN-2005 (first entry)
XX Enterococcus faecalis vanB DNA sequence SEQ ID NO:15.
XX

KW DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
XX Enterococcus faecalis.
XX US2005058985-A1.
XX PN 17-MAR-2005.
XX PD 12-SEP-2003; 2003US-00661094.
XX PF 12-SEP-2003; 2003US-00661094.
XX PR 12-SEP-2003; 2003US-00661094.
XX PA (DODG/) DODGSON K J.
XX PI Dodgson KJ;
XX DR WPI; 2005-222218/23.
XX PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT and/or vanB-specific oligonucleotide probes or primers.
XX PS Example 1; SEQ ID NO 15; 33pp; English.
XX CC The invention relates to a method for detecting vancomycin resistance
CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
CC probe or primer, and detecting or determining the presence or amount of
CC hybrid formation or amplified nucleic acid. Also described: (1) an
CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 898-917 of the vanA gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC vanB gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents an
CC Enterococcus faecalis vanB nucleotide sequence from the present
CC invention.
XX SQ Sequence 630 BP; 163 A; 135 C; 187 G; 145 T; 0 U; 0 Other;
Query Match 76.3%; Score 20.6; DB 14; Length 630;
Best Local Similarity 85.2%; Pred. No. 24;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
Db 185 CCTACCTGTCTTGTGTAAGCCGCGAC 211
RESULT 34
ADY59942
ID ADY59942 standard; DNA; 783 BP.
XX AC ADY59942;
XX DT 02-JUN-2005 (first entry)
XX DE Enterococcus faecalis vanB DNA sequence SEQ ID NO:16.
XX KM DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
XX OS Enterococcus faecalis.
XX PN US2005058985-A1.

XX 17-MAR-2005.
XX PD 12-SEP-2003; 2003US-00661094.
XX PF 12-SEP-2003; 2003US-00661094.
XX PR 12-SEP-2003; 2003US-00661094.
XX PA (DODG/) DODGSON K J.
XX PI Dodgson KJ;
XX DR WPI; 2005-222218/23.
XX PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT and/or vanB-specific oligonucleotide probes or primers.
XX PS Example 1; SEQ ID NO 16; 33pp; English.
XX CC The invention relates to a method for detecting vancomycin resistance
CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
CC probe or primer, and detecting or determining the presence or amount of
CC hybrid formation or amplified nucleic acid. Also described: (1) an
CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 898-917 of the vanA gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC vanB gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents an
CC Enterococcus faecalis vanB nucleotide sequence from the present
CC invention.
XX SQ Sequence 783 BP; 215 A; 166 C; 223 G; 179 T; 0 U; 0 Other;
Query Match 76.3%; Score 20.6; DB 14; Length 783;
Best Local Similarity 85.2%; Pred. No. 24;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
Db 392 CCTACCTGTCTTGTGTAAGCCGCGAC 418
RESULT 35
AAH01126
ID AAH01126 standard; DNA; 801 BP.
XX AC AAH01126;
XX DT 24-JUL-2001 (first entry)
XX DE Enterococcus faecium nucleotide sequence SEQ ID NO:1117.
XX KM Species specific; genus specific; family specific; probe; detection;
KM identification; algal; archaeal; bacterial; fungal; parasitic;
KM microorganism; diagnosis; translation elongation factor Tu; toxin;
KM translation elongation factor G; RecA recombinase; resistance;
KM catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
KM primer; ds.
XX OS Enterococcus faecium.
XX PN WO200123604-A2.

XX 05-APR-2001.
PD 28-SEP-2000; 2000WO-CA001150.
XX 28-SEP-1999; 99CA-02283458.
XX 19-MAY-2000; 2000CA-02307010.
XX (INPR-) INFECTIO DIAGNOSTIC (IDT) INC.
XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX WPI; 2001-24506/25.
DR Nucleic acid sequences are used to generate universal probes and primers
PT which can be used to identify and detect the presence of algal, archaeal,
PT bacterial, fungal and parasitic species in a test sample.
XX Disclosure; Page 1027; 1580pp; English.
XX The present invention describes a method for generating a repository of
XX nucleic acids of tuf, fus, atpD and/or recA genes from which probes
XX and/or primers are derived. The method comprises amplifying the nucleic
XX acids of determined algal, archaeal, bacterial, fungal and parasitic
XX species with a combination of defined primer pairs. The method can be
XX used for producing probes and/or primers for detecting one or more
XX related microorganisms e.g. algae, archaea, bacteria, fungi and
XX parasites, for universal detection and for specific and ubiquitous
XX detection and identification of an algal, archaeal, bacterial, fungal and
XX parasitic species, genus, family and group. A nucleic acid (I) obtained
XX using the method of the invention can be used for the universal detection
XX of any bacterium, fungus or parasite in a sample and for the detection of
XX at least one antimicrobial agent resistance gene or at least one toxin
XX gene. hexA nucleic acids are used for the specific and ubiquitous
XX detection and for identification of Streptococcus pneumoniae. (I) can be
XX used to design a therapeutic agent which is effective against
XX microorganisms. Microbial species or genus or family or phylum or group
XX which can be detected include Abiotrophia adiacens, Bordetella sp.,
XX Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
XX Mycobacteriaceae family, Pseudomonas group, Streptococcus sp., Neisseria
XX gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster
XX results than substrate specificity tests as results can be determined in
XX an hour and improved accuracy is also achieved. AAH00010 to AAH002304
XX represent nucleotide sequences and primers/probes which are given in the
XX exemplification of the present invention
XX
XX Sequence 801 BP; 215 A; 169 C; 235 G; 182 T; 0 U; 0 Other;
SQ
XX
XX Query Match 76.3%; Score 20.6; DB 4; Length 801;
XX Best Local Similarity 85.2%; Pred. No. 25;
XX Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
DB 389 CCTACCTGTCTTGTGTAAGCCGCGAC 415
XX
XX RESULT 36
XX ADY59937/c
XX ID ADY59937 standard; DNA; 801 BP.
XX AC ADY59937;
XX XX
XX 02-JUN-2005 (first entry)
XX DE Enterococcus faecium vanB DNA sequence SEQ ID NO:11.
XX XX
XX DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
XX KM Enterococcus faecium.
XX OS
XX PN US2005058985-A1.

XX 17-MAR-2005.
PD 12-SEP-2003; 2003US-00661094.
XX 12-SEP-2003; 2003US-00661094.
XX 12-SEP-2003; 2003US-00661094.
XX (DODG/) DODGSON K J.
XX Dodgson KJ;
XX WPI; 2005-222218/23.
XX
XX Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
XX e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
XX and/or vanB-specific oligonucleotide probes or primers.
XX Example 1; SEQ ID NO 11; 33pp; English.
XX
XX The invention relates to a method for detecting vancomycin resistance
XX gene vanA and/or vanB nucleic acid molecules in a sample comprising
XX contacting the sample with a vanA- and/or vanB-specific oligonucleotide
XX probe or primer, and detecting or determining the presence or amount of
XX hybrid formation or amplified nucleic acid. Also described: (1) an
XX oligonucleotide composition comprising a first oligonucleotide comprising
XX sequences substantially corresponding to nucleotides 870-896, 851-868 or
XX 898-917 of the vanA gene, or its complement or portion, or an
XX oligonucleotide comprising sequences substantially corresponding to
XX nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
XX complement or portion, where the oligonucleotide hybridizes under
XX stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
XX comprising one or more oligonucleotide(s) specific for a vanA gene and/or
XX vanB gene in a test sample, comprising the oligonucleotide mentioned
XX above. The method and kit are useful for detecting and/or amplifying
XX genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
XX antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
XX They may also be used in other industrial purposes, such as for quality
XX control of food, water, pharmaceutical products or other products
XX requiring microbiological control. The present sequence represents an
XX Enterococcus faecium vanB nucleotide sequence from the present invention.
XX
XX Sequence 801 BP; 181 A; 226 C; 169 G; 225 T; 0 U; 0 Other;
SQ
XX
XX Query Match 76.3%; Score 20.6; DB 14; Length 801;
XX Best Local Similarity 85.2%; Pred. No. 25;
XX Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
DB 413 CCTACCTGTCTTGTGTAAGCCGCGAC 387
XX
XX RESULT 37
XX ADY59940/c
XX ID ADY59940 standard; DNA; 801 BP.
XX AC ADY59940;
XX XX
XX 02-JUN-2005 (first entry)
XX DE Enterococcus faecium vanB DNA sequence SEQ ID NO:14.
XX XX
XX DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
XX KM Enterococcus faecium.
XX OS
XX PN US2005058985-A1.
XX 17-MAR-2005.
XX 12-SEP-2003; 2003US-00661094.
XX 12-SEP-2003; 2003US-00661094.
XX 12-SEP-2003; 2003US-00661094.

XX (DODG/) DODGSON K J.
 XX
 PA Dodgson KJ;
 PI
 XX WPI; 2005-222218/23.
 XX
 PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
 PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
 PT and/or vanB-specific oligonucleotide probes or primers.
 XX
 PS Example 1; SEQ ID NO 14; 33pp; English.
 XX
 PS The invention relates to a method for detecting vancomycin resistance
 CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
 CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
 CC probe or primer, and detecting or determining the presence or amount of
 CC hybrid formation or amplified nucleic acid. Also described: (1) an
 CC oligonucleotide composition comprising a first oligonucleotide comprising
 CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
 CC 898-917 of the vanA gene, or its complement or portion, or an
 CC oligonucleotide comprising sequences substantially corresponding to
 CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
 CC complement or portion, where the oligonucleotide hybridizes under
 CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
 CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
 CC vanB gene in a test sample, comprising the oligonucleotide mentioned
 CC above. The method and kit are useful for detecting and/or amplifying
 CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
 CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
 CC They may also be used in other industrial purposes, such as for quality
 CC control of food, water, pharmaceutical products or other products
 CC requiring microbiological control. The present sequence represents an
 CC Enterococcus faecium vanB nucleotide sequence from the present invention.
 XX
 SQ Sequence 801 BP; 183 A; 234 C; 169 G; 215 T; 0 U; 0 Other;
 XX
 QY Query Match 76.3%; Score 20.6; DB 14; Length 801;
 DB Best Local Similarity 85.2%; Pred. No. 25;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CCGATCCTGTTTGTGTAAGCCGCGC 27
 DB 413 CCGATCCTGTTTGTGTAAGCCGCGCAC 387
 XX
 RESULT 38
 ADY59943/c
 ID ADY59943 standard; DNA; 801 BP.
 XX
 AC ADY59943;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE Consensus vanB DNA sequence SEQ ID NO:14.
 XX
 KM DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
 XX
 OS Enterococcus faecium.
 OS Enterococcus faecalis.
 OS Synthetic.
 XX
 PN US2005058985-A1.
 XX
 PD 17-MAR-2005.
 XX
 PF 12-SEP-2003; 2003US-00661094.
 XX
 PR 12-SEP-2003; 2003US-00661094.
 XX
 PA (DODG/) DODGSON K J.
 XX
 PI Dodgson KJ;

XX WPI; 2005-222218/23.
 XX
 DR Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
 XX PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
 PT and/or vanB-specific oligonucleotide probes or primers.
 PT
 XX
 PS Example 1; SEQ ID NO 17; 33pp; English.
 XX
 PS The invention relates to a method for detecting vancomycin resistance
 CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
 CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
 CC probe or primer, and detecting or determining the presence or amount of
 CC hybrid formation or amplified nucleic acid. Also described: (1) an
 CC oligonucleotide composition comprising a first oligonucleotide comprising
 CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
 CC 898-917 of the vanA gene, or its complement or portion, or an
 CC oligonucleotide comprising sequences substantially corresponding to
 CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
 CC complement or portion, where the oligonucleotide hybridizes under
 CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
 CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
 CC vanB gene in a test sample, comprising the oligonucleotide mentioned
 CC above. The method and kit are useful for detecting and/or amplifying
 CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
 CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
 CC They may also be used in other industrial purposes, such as for quality
 CC control of food, water, pharmaceutical products or other products
 CC requiring microbiological control. The present sequence represents a
 CC consensus vanB nucleotide sequence from the present invention.
 XX
 SQ Sequence 801 BP; 181 A; 235 C; 169 G; 216 T; 0 U; 0 Other;
 XX
 QY Query Match 76.3%; Score 20.6; DB 14; Length 801;
 DB Best Local Similarity 85.2%; Pred. No. 25;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CCGATCCTGTTTGTGTAAGCCGCGC 27
 DB 413 CCGATCCTGTTTGTGTAAGCCGCGCAC 387
 XX
 RESULT 39
 ADY59939/c
 ID ADY59939 standard; DNA; 801 BP.
 XX
 AC ADY59939;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE Enterococcus faecium vanB DNA sequence SEQ ID NO:13.
 XX
 KM DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
 XX
 OS Enterococcus faecium.
 OS Enterococcus faecalis.
 OS Synthetic.
 XX
 PN US2005058985-A1.
 XX
 PD 17-MAR-2005.
 XX
 PF 12-SEP-2003; 2003US-00661094.
 XX
 PR 12-SEP-2003; 2003US-00661094.
 XX
 PA (DODG/) DODGSON K J.
 XX
 PI Dodgson KJ;
 XX
 DR WPI; 2005-222218/23.
 XX
 PT Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
 PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
 PT and/or vanB-specific oligonucleotide probes or primers.

XX Example 1; SEQ ID NO 13; 33bp; English.
PS
XX The invention relates to a method for detecting vancomycin resistance
CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide
CC probe or primer, and detecting or determining the presence or amount of
CC hybrid formation or amplified nucleic acid. Also described: (1) an
CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 898-917 of the vanA gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC vanB gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents an
CC Enterococcus faecium vanB nucleotide sequence from the present invention.
XX
SQ Sequence 801 BP; 183 A; 234 C; 169 G; 215 T; 0 U; 0 Other;
Query Match 76.3%; Score 20.6; DB 14; Length 801;
Best Local Similarity 85.2%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
DB 413 CCTACCTGCTTTGTGTAAGCCGCGC 387
RESULT 40
ADYS9936/c
XX ID ADYS9936 standard; DNA; 801 BP.
XX AC
XX ADYS9936;
XX
DT 02-JUN-2005 (first entry)
XX
XX Enterococcus faecium vanB DNA sequence SEQ ID NO:10.
DE
XX DNA detection; antibiotic-resistance; vancomycin; vanB; ds.
KM
XX Enterococcus faecium.
OS
XX US2005058985-A1.
PN
XX 17-MAR-2005.
PD
XX 12-SEP-2003; 2003US-00661094.
PF
XX 12-SEP-2003; 2003US-00661094.
PR
XX (DODG/) DODGSON K J.
PA
XX Dodgson KJ;
PI
XX WPI; 2005-222218/23.
DR
XX
XX Detecting vanA and/or vanB nucleic acid molecules in a sample, useful for
PT e.g. identifying vancomycin-resistant enterococcus, comprises using vanA-
PT and/or vanB-specific oligonucleotide probes or primers.
XX
XX Example 1; SEQ ID NO 10; 33bp; English.
PS
XX The invention relates to a method for detecting vancomycin resistance
CC gene vanA and/or vanB nucleic acid molecules in a sample comprising
CC contacting the sample with a vanA- and/or vanB-specific oligonucleotide

CC probe or primer, and detecting or determining the presence or amount of
CC hybrid formation or amplified nucleic acid. Also described: (1) an
CC oligonucleotide composition comprising a first oligonucleotide comprising
CC sequences substantially corresponding to nucleotides 870-896, 851-868 or
CC 898-917 of the vanA gene, or its complement or portion, or an
CC oligonucleotide comprising sequences substantially corresponding to
CC nucleotides 387-404, 406-423 or 426-446 of the vanB gene, or its
CC complement or portion, where the oligonucleotide hybridizes under
CC stringent hybridization conditions to vanA or vanB DNA; and (2) a kit
CC comprising one or more oligonucleotide(s) specific for a vanA gene and/or
CC vanB gene in a test sample, comprising the oligonucleotide mentioned
CC above. The method and kit are useful for detecting and/or amplifying
CC genes (i.e. vanA and/or vanB genes) in a test sample, or for identifying
CC antibiotic resistance genes (e.g. vancomycin-resistant enterococcus).
CC They may also be used in other industrial purposes, such as for quality
CC control of food, water, pharmaceutical products or other products
CC requiring microbiological control. The present sequence represents an
CC Enterococcus faecium vanB nucleotide sequence from the present invention.
XX
SQ Sequence 801 BP; 182 A; 235 C; 169 G; 215 T; 0 U; 0 Other;
Query Match 76.3%; Score 20.6; DB 14; Length 801;
Best Local Similarity 85.2%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CCTATCCTGTTTGTGTAAGCCGCGC 27
DB 413 CCTACCTGCTTTGTGTAAGCCGCGC 387
Search completed: April 9, 2006, 06:41:33
Job time : 381.134 secs

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